

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 96683

TO: Minh-Tam Davis

Location: CM1/8A01/8E12

Art Unit:, 1642

6/18/03 20

2003

Case Serial Number: 991681

From: P. Sheppard Location: CM1-1E03 Phone: (703) 308-4499

sheppard@uspto.gov

#### Search Notes

Provide clate: 47/98 024/97?

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#### STIC-Biotech/ChemLib

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From: Sent: To:

Subject:

Davis, Minh-Tam Monday, June 16, 2003 3:28 PM STIC-Biotech/ChemLib Search request for 09/991681

Please search in commercial database, PGPUB and issued patent files: SEQ ID NO:27-31. Thank you. MINH TAM DAVIS ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Point of Contact P. Sheppard Telephone number: (703) 308-4499

·	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
ocation:	Structures:	Questel/Orbit:
Date Picked Up: ///	Bibliographic:	DRLink:
Date Completed 6/8/03	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 66.4 kDa protein (Fragment).
Homo Sapiens (Human).
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Mammalia; Eutheria;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M.A., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M.A., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M.A., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M.A., Pfeiffer B.D.,

RA George R.A., Lewis S.E., Richards G., Champè M., Pfeiffer B.D.,

RA George R.A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champè M., Pfeiffer B.D.,

RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Apbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botsam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Borkova D., Bolsam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Riner M., Malshina R., Pan S., Pollar
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Múscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                               63.5
61
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length: 2000000000
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Gapop 10.0 ,
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215
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Match
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100.0
100.0
30.2
29.8
29.5
29.5
27.4
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                       sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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                                                                                                                                                                        Q96CH9
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Q59301
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                      Q9FT44
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Q929Z6
Q8XBF3
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Q8S341
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                                                                       Q9ft44 arabidopsis
Q8u805 agrobacteri
Q94im7 hordeum vul
Q929z6 listeria in
Q8xbf3 escherichia
                                                                                                                                                Q96ch9
Q9u1h6
Q9bje8
Q59301
                    064951 tagetes ere
064950 tagetes ere
09sis6 arabidopsis
08s341 arabidopsis
                                                                                                                                    Q59301 cellvibrio
Q74491 schizosacch
                                                                                                                                                                                                            Description
           Q918p3 haemophilus
                                                                                                                                                                          homo sapien
homo sapien
                                                                                                                                                              plasmodium
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45	44	43	42	41	40	39	ა 8	37	36	ယ 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
52	52.5	52.5	52.5	52.5	53	53	53	53	53	53	53	53	53	53	53	53	53.5	53.5	54	54	54.5	54.5	55	55	55	55		55.5
24.2	24.4	24.4	24.4	24.4	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	•	•	24.9	•	25.1	25.3	25.3	25.6	25.6	25.6	25.6	25.6	25.8
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Q9D068	Q9WZ87	Q9BDV9	Q8X1E4	Q9S7C4	Q9FK71	Q21136	Q9NUQ3	Q9VFF6	Q8VJU6	007732	Q9FK39	Q9SZX1	Q8RUE5	Q93905	Q9P0X1	Q9BJF0	Q9LIV9	Q93EX6	004938	Q8VP74	Q94 IM6	Q9AV96	Q9FLI2	Q9MB29	Q9SMB7	Q9SMC1	024127	Q9N4T5
Q9d068 mus musculu		~		Q9s7c4 hevea brasi		റ				mycobacter				` ^		Q9bjt0 plasmodium		Q93ex6 rhodococcus	œ	Q8vp74 pseudomonas	Q94im6 hordeum vul						024127 nicotiana t	Q9n4t5 caenorhabd1 .

### ALIGNMENTS

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RESULT 1
Q96CH
Q96CA
AC Q96C
AC Q96CA
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Q9ULH6
                                               BARARE
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Best Local Similarity
Matches 40; Conserv
Q9ULHS, Q96P46;
Q9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 66.4 kDa protein (Fragment).
Hymon sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014227; AAH14227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                         Q9ULH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96СН9;
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                                                                                                                                                                                                                                                                                                                                                                                                                          592 AA; 66400 MW; F4A1E807B0DF47B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                         PRELIMINARY;
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100.0%; Pred. No. 6e-20;
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Best Local
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                                                                                                                          NON_TER
                                                                                                                                        *Khattab A., Kun J., Deloron P., Kremsner P.G.,

*Variants of Plasmodium falciparum Erythrocyte

Expressed by Different Placental Parasites are

Adhere to Chondroitin Sulfate A.*,

Infect. Dis. 183:1165-1169(2001).

EMBL; AF334805; AAK28128.1;
                                                                                                             SEQUENCE
                                                                                                                                                                                                                       MEDLINE=21136462; PubMed=11237850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "KIAA1244 as a novel distantly related member (BIG3) of the subfamily of ARF GEFs.", Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB033070; BAA86558 1; EMBL; AF413080; AAL04174.1; InterPro; IPR000904; Sec7; 1.
SMART; SM00222; Sec7; 1.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 Plasmodium falciparum.

Plasmodium falciparum.

Rukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium

RUBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=20039619; PubMed=10574462; Ragase T., Ishikawa K., Kikuno R., Hirosawa M., Nomu Prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from b I large proteins in vitro."; Res. 6:337-345(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                     JUN-2001
JUN-2001
JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 38-1807 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              ythrocyte membrane protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1621
112 KKDDTKRKEWWENNKSHIW
                       6 KKDPSRKKEWWENAGNKIY 24
                                                        l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity.
                                                                                                         177
177 AA;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1807 AA;
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                        21207 MW;
                                                              30.2%; Score 65; 1
52.6%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199921 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 215; DB 4;
Pred. No. 2.1e-19;
Mismatches 0;
                                                                                                 318AC7FFEF0102A2 CRC64;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B762C29916F72CB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  177
                                                              DB 5;
0.89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo
                                                                        Length 177;
                                                                                                                                                                                       Klinkert M.Q.;
Membrane Protein 1
                                                                                                                                                                             Membrane Proteir
Closely Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nomura N., Ohara O.;
fied human genes. XV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1807;
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brain w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which code
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059301

PRELIMINARY;

PRT;

621

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HSSP: P14768; 1CLX.
HSSP: P14768; 1CLX.
InterPro; IPR005088; CBM_15.
R InterPro; IPR001000; Glyco_hydro_10.
R Pfam; PP03426; CBM_15; 1.
JR Pfam; PP00331; Glyco_hydro_10; 1.
DR PRINTS; PP00134; GLYCOLYDRLASE10.
DR PRINTS; PR00134; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
Glycosidase; Hydrolase; Signal; Xylan degradation.
FOTENNAL 1 19
FOTENTIAL CTCNAL 1 19
FOTENTIAL 1 1 19

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Best Local S
DNA Res. 4:363-369(1997)
-!- SIMILARITY: TO OTHER "DEAD" BO
EMBL; AL031545; CAA20842.1; -
EMBL; D89259; BAA13920.1; -
InterPro; IPR001410; DEAD
InterPro; IPR001679, DEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                WEDLINE-98162722; PubMed-9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces
CDNAs.";
                                                                                                                                                                                                                                                           SEQUENCE OF 115-604 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            074491; p78908;
01-NOV-1998 (TrEMBLrel 08, Created)
01-NOV-1998 (TrEMBLrel 08, Last sequence update)
01-NOV-2998 (TrEMBLrel 20, Last annotation update)
Putative ATP-dependent RNA helicase C285.03.
                                                                                                                                                                                                                                                    STRAIN-PR745
                                                                                                                                                                                                                                                                                                                                                               STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                             eeger K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Millward-Sadler S.J., Davidson K., Hazlew Gilbert H.J., Clarke J.H.,
"Novel cellulose-binding domains, NodB ho modular architecture in xylanases from th Pseudomonas fluorescens subsp. cellulosa Biochem. J. 312:39-48[1995].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    059301;
01-NOV-1996
01-NOV-1996
01-JUN-2002
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HSSP; P14768; 1CLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadâceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Endo-beta-1,4-xylanase precursor (EC 3.2.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96077124; PubMed-7492333;
Millward-Sadler S.J., Davidson K., Hazlewood G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 PIVQIKGGSYPGEWGCWAGNELFTAGEDATISCTVTE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascomycota; Schizosaccharomycete
etales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
43.2%;
                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                           Lyne M., to the EMT
                                                                                                                                                                                                                                                                                              M., Rajandream M.A., Barrell B.G.; EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB;
Pred. No. 4.9;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomycetes;
                                                                                  BOX FAMILY HELICASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NodB homologues and conserved from the aerobic soil bacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellvibrio mixtus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 621;
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Result
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                         Score
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Match
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1: /SIDS2/gcgdata/c
2: /SIDS2/mmm
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Gapop 10.0 ,
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989 DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990 DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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   AAM50813
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AAM509728
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AAU32052
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AAM61151
AAM73865
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the result bein
distribution.
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                                                                                               PS118 prostate mar
PS118 prostate mar
PS118 prostate mar
Novel human diagno
Novel human diagno
Novel human secret
Peptide #7852 enco
                                                                                                                                                                                                                                                                                                                                                                                      Description
Human brain expres
Human bone marrow
Peptide #8084 enco
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being pr
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RESULT 1
AAMSO813
ID AAMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS118 prostate marker immunogenic polypeptide
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Peptide #11327 enc	ABB43821	22	70	21.5	
3	AAU87071	23	313	21.7	
Mutated thymidylat	7576	19	313	21.7	9
ed thymic	576	19	313	21.7	6
thymic	576	19	313	21.7	6
ted thymidyla	576	19	313	21.7	5
ted thymidyla	576	19	313	21.7	σ,
ted thymidyla	576	19	313	21.7	σ.
thymidyla	576	19	313	21.7	6
ted 1	576	19	313	21.7	9
ted thymidyla	576	19	313	$\vdash$	σ,
ted thymidyla	AAW75759	19	313	21.7	56.5
ted thymidyla	75	19	313	21.7	5
ted	575	19	313	$\vdash$	5
	575	19	313	1	5
ed	575	19	313	:	5
ת ב	077	22	189	Ξ.	6
ع	368	22	558	:	57
prote	997	22	514	1.	57
	999	22	495	1.	57
acid			485	1	57
o			485	۲.	57
Novel human diagno			331	7	57
Human foetal prote	AAM06884		152	1.	57
Encoded by human G			83	<u>.                                    </u>	57
Arabidopsis thalia			79	۳.	57
Arabidopsis thalia			71		57
Mutated thymidylat	575	19	313	2	7.
Mutated thymidylat	575	19	313	۲	7.
phila me	Ē	22	3429	2	58.5
Human 1mmune/haema	490	22			œ
ibacterium	6615	22		۲.	
ne mammary	765	22	87	ω.	
l human	G2225	22	171	24.2	63
Human peptide enco	ABG43753	23	70		

### ALIGNMENTS

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(first entry)

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(BILL) BILLING-MEDEL P A. (COHE) COHEN M. (COPL) COPLPITTS T L. (FRIE) FRIEDMAN P N. (GORD) GORDON J. (GRAN) GRANADOS E N. (HODG) HOOGES S C. (KLAS) KLASS M R. (KRAT) KRATOCHVIL J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                     23-APR-1998;
                                                                                                                                                                                                                                                                                                                                    27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                       23-APR-1997;
                                                                                                                                                                                                                                       97US-0842385
                                                                                                                                                                                                                                                                                     98US-0065383
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comprising amino acids 393-441 of human prostate-specific PS118 CC polypeptide (see AAM50809). A PS118 consensus sequence (see CC ABA91651) is found at least 12 times more often in prostate tissue. PS118 polypeptides, polypucleotides, agonists and inhibitors are useful for detecting, CC diagnosing, staging, monitoring, prognosticating, preventing and CC treating (including by genetic immunisation), or determining the CC prostate, such as benign prostatic hyperplasia, prostatic candidate, such as benign prostatic hyperplasia, prostatic tuntraepithelial neoplasia, prostate cancer, tumours and CC ef PS118 polypucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of invention may provide an open contents.
                                                                                                                                                                                                                                                                                                                                        RESULT 2
AAW85472
  PIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멂
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                Gordon
                           Billing-Medel PA,
                                                                                  23-APR-1997;
                                                                                                          23-APR-1998;
                                                                                                                                                                                                                                                                                                                            AAW85472 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies of diagnostic use. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROBE/) ROBERTS-RAPP L.
 Robert-Srapp L,
                                                     (ABBO ) ABBOTT
                                                                                                                                      29-OCT-1998
                                                                                                                                                               W09848054-A1
                                                                                                                                                                                                                    EST clone;
                                                                                                                                                                                                                                           PS118 protein encoded by consensus sequence.
                                                                                                                                                                                                                                                                         25-FEB-1999
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                without the use of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                       EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                    PS118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
                Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  el PA, Cohen
, Hodges SC,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                       LAB
                                                                                  97US-0842385
                                                                                                          98WO-US08239
  Russell
                             Cohen M,
                                                                                                                                                                                                                  prostate
                                                                                                                                                                                                                                                                                                                            Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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M, Colpitts TL,
Hodges SC, Klas
JC, Stroupe SD;
                                                                                                                                                                                                                    tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 1.3e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                  tissue;
             Klass MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kratochvil JD,
                                                                                                                                                                                                                  prostatic
                           Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman PN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
               Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts-Rapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon J;
               ď,
                                                                                                                                                                                                                                                                                                                                                                                                                       49
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AAM50809
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Best Local
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of used for detection, diagnosis, staging, monitoring and prognosis of potential disease, particularly cancer, and to identify subjects at
                                                                                                                                                                          (BILL/)
                                Billing-Medel PA,
Granados EN, Hod
                                                                                                                                                                                                                                                                                          US2001055758-A1.
                                                                                                                                                                                                                                                                                                                                                                 PS118; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM50809 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New P118 nucleic acid and proteins - treatment of prostatic disease, espec
                       Russell
                                                                                                                                                                                                                 23-APR-1997;
                                                                                                                                                                                                                                        23-APR-1998;
                                                                                                                                                                                                                                                                 27-DEC-2001.
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       benign
                                                                                                                                                                                                                                                                                                                                                                                            PS118 prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM50809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            risk.
                                                                         (ROBE/)
                                                                                                                           (GRAN/)
                                                                                                                                                                (COPL/)
                                                                                      KRAT
                                                                                                  KLAS/)
                                                                                                              HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-610000/51.
DB; AAV82812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                     KLASS M R.
) KRATOCHVIL J D.
CORRERS-RAPP L.
                                                                                                                                                                                                                                                                                                                                        prostate; marker; prostate cancer; tumour; metastasis;
prostatic hyperplasia; prostatic intraepithelial neopl
titis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                           GRANADOS E N. HODGES S C.
                                                                                                                                                COPLPITTS T L. FRIEDMAN P N.
                                                                                                                                       GORDON J.
                                                                                                                                                                                     BILLING-MEDEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                            COHEN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518
                     Hodges
Stroupe
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          marker partial
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                                                                                                                                                                                                                 97US-0842385
                                                                                                                                                                                                                                        98US-0065383
                      Cohen
ges SC,
upe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and proteins - used for diagnosis disease, especially cancer, and a
                                   M, Coplpitts TL, Friedman PN, Klass MR, Kratochvil JD, Rob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 260; DB 19;
Pred. No. 2.1e-27;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                    intraepithelial neoplasia;
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                                  Roberts-Rapp L;
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                                                Gordon J;
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WPI; 2002-187683/24

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RESULT 4
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              including derivatives of the present sequence, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and interportant programs of the prostate and may also provide new markers which can differentiate between the clinically important and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease.
                                                              WPI; 2001-639362/73
N-PSDB; AAS73915.
                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                  30-MAR-2001;
                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #9719
                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG09728 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see ABA91651), and lacking the N-terminal region. The F consensus sequence is found at least 12\ \text{times} more often
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide, as (see ABA91651),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
New isolated polynucleotide and encoded polypeptides, using diagnostics, forensics, gene mapping; identification of responsible for genetic disorders or other traits and to
                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate than in non-prostate tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is
                                                                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                        HYSEQ
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                                                                                                          RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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2000US-0649167
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                                                                                                                                        INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that of a human prostate-specific PS118 ed from a partial consensus cDNA sequence king the N-terminal region. The PS118
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Pred. No. 2.1e-27;
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                                useful in
                  mutations
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RESULT 5
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CC Mote: The sequence data for this patent did not appear in the printed conception of the concept of the sequence of the invention.

CC at fix wipo.int/pub/published_pct_sequences.
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               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #9722
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                                                                                                                                            Drmanac
                                                                                                                                                                                                                                                                                             11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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)B; AAS73918.
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                                                                                                                                            RT,
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                                                                                                                                                                                                             2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 9e-
); Mismatches
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                                               mutations
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopolesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
 The invention relates to novel human secreted polypeptides. polypeptides and antibodies to the polypeptides are useful
                                                                                    Nucleic acids encoding a vaccination, testing and
                                                                                                                                         WPI; 2001-611725/70.
                                                                                                                                                                                                                                           18-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromos and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence
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                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                                                                                                              25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                              WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human
                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                   20; Page 548-549; 765pp; English
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                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1982 AA;
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2001US-0770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                      range of human polypeptides, useful in genetic therapy -
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Pred. No.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
   nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising
           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exonucleic acid probe of the invention.
                                                                                                                            Claim
                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #7852 encoded by human foetal liver single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
                                                                                                                                                                                                        2001-483447/52
                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 GKNGQGEPAVVRCSHLL----VKHSQSRRPSSWRQEKITRTKGGGPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDK--RPRSGSTGS
                                                                                                                          SEQ
 sequence data
                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                                                                                                                               2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312
2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                            2000US-0608408
                                                                                                                          ID NO 32981; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.8%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression;
                                                                                                                                                                                                                                     Chen
   for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 2
Pred. No. 0.37;
                                                                                                                                                                                                                                     Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
   patent did not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6,
                                              from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 8
AAM61151
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В
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                                      Query Match
Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                          Sequence
                                                                                                      diseases such as Alzheimer's epilepsy and cancers. The pro
                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                                       Example 4;
                                                                                                                                                                                                 Single
                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                          WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM61151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM61151 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                            probes
                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                     2001-483446/52
                                                                                                                                                                                                                                       SG,
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   12
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19; Conserv
                                                Similarity
                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRGQDSPLLQRPQHLMDQGQMRHSFSA-----GP------
                   PRGQDSPLLQRPQHLMDQGQMRHSFSA-----GP-----ELLRQDKRPRSGSTG
                                                                                                                                                                                                                                       Hanzel
                                                                                                                                                                       SEQ
                                                                           70
                                                                                             of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AA;
                                                                                                                                                                                                                                                                                 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                  nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                    2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                            2000GB-0024263
                                                                           A,
                                                                                                                                                                       ID NO:
                                                                                                                                                                                                                                      DK,
 -QQPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%;
                                                24.2%;
                                                                                                      The present
                                                                                                                                                                                                                                       Chen
                                                                                                                                                                      33256; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63;
Pred. No.
                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                 disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                       Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                 for analyzing gene expression
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis; so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe encoded protein
                                                                                                      sequence
                                                No.
                                                                                                                                                                                                                                       DR;
                                                                                                       multiple
|uence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                DB 22;
0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                       13;
                                                                                                       D
                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                        Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELLRODKRPRSGSTG
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        schizophrenia;
                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                       encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO:
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                                      Gaps
                                                                                                       by one
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   61
                    48
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RESULT 9
AAM73865
ID AAM7
                                                                                                          RESULT 10
AAM34047
ID AAM34
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                                                                                                                                                                                                    Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM73865 standard; Protein; 70
                   Probe; microarray;
genetic disorder.
                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM73865;
                                                                     17-OCT-2001
                                                                                         AAM34047;
                                                                                                             AAM34047 standard;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                      Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
                                                 Peptide #8084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                        2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes
                                                                                                                                                              12
                                                                                                                                                                                  G
                                                                                                                                                                                                      l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                              PPGQ-----QQPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG
                                                                                                                                                                                PRGQDSPLLQRPQHLMDQGQMRHSFSA----GP----
                                                                                                                                                                                                                                                                                                                                                          gene expression
                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel
                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234685.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US00668
                                                encoded by probe
                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                      ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed
                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed
                             human;
                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia;
                                                                                                                                                                                                              24.28;
                                                                                                                                                                                                                                                                                                                                      34171; 658pp + Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                            placenta;
                                                                                                                                                                                                                                                                                                                                                          in human bone marrow
                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe
                                                                                                                                                                                                    Score 63; DB Pred. No. 0.4; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon;
                                                                                                             A
A
                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                 for measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression
                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                             antenatal
                                                                                                                                                                                                                 .4
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                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                      Listing; English
                                                                                                                                                                                                                          Length 70
                                                                                                                                                                                  ELLRODKRPRSGSTG
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                     useful
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                                                                                                                                                                                                      16;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                       Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; single exon probe; asthma; lung cancer; COPD; IID; chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 34316; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001;
                                                                                                              15-NOV-2001
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide encoded by genome-derived single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG43753 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
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                                                     30-JAN-2001; 2001WO-US00665
                                                                                                                                                                      WO200186003-A2
                                                                                                                                                                                                                                                                                                                     primary ciliary dyskinesis; pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                       membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGQ-----QQPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AA;
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2000US-180312P
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2000GB-0024263.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                       disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB:
Pred. No. 0.4;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease;
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RESULT 12 ABG22251

ABG22251 standard; Protein; 171

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                                                                                            Best Loc
Matches
                                                                                                                                     Query Match
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                    haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener Syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypert and hyaline membrane disease. The present sequence is a peptide/pi encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                     of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Nemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary hasmann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample deriv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes for measuring gene expression from human lung comprising single exon nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
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  12
                                           5 PRGQDSPLLQRPQHLMDQGQMRHSFSA-----GP-----ELLRQDKRPRSGSTG 48
                                                                                            l Similarity
19; Conser
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2000US-234687P.
2000US-236359P.
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2000US-0608408
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-QQPPHLHHRGGRRHSEAVHSHRPGPGVRIHLQAVRQDEAGLGGATG
                                                                                                                 24.2%;
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                                                                                                               Score 63;
Pred. No.
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                                                                                            Mismatches
                                                                                                               DB 3
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                                                                                                                                          23;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The C polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity and considered types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human and assess biodiversity this natural did not annear in the printed considers the polyment of the products dependent on DNA and CC diagnostic amino acid sequences of the invention.
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                                                                     AAB87657 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 52610; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                     PLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTG 48
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                  protein; 87
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Mismatches 7
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RESULT 14
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   21-APR-2000; 2000US-199047P
                                                              20-APR-2001; 2001WO-US12865
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Query Match
Best Local
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                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomy uveitis; endophthalmitis; bone; joint; central nervous system; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting angiogenesis and vascularization of tumours, or modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 80; 97pp; English.
Propionibacterium
                                                                                                                                    Propionibacterium acnes immunogenic protein #27052
                                                                                                                                                                             27-FEB-2002
                                                                                                                                                                                                                     AAU66156;
                                                                                                                                                                                                                                                            AAU66156 standard;
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                                     dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the growth of blood vessels in a mammal.
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(NZPA-) NEW ZEALAND PASTORAL AGRIC
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                                                                                                                                                                             (first entry)
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                                   osteopathic;
                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cc sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The cc polypeptides may be used as antigens in the production of antibodies specific for P. acnes porteins. These antibodies can be used to compregulate expression and activity of P. acnes polypeptides and cc therefore treat P. acnes infections. The antibodies may also be used as consequence inked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed consequence in the internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino internal obtained in electronic format directly from WIPO at the wino in the win
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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07-JUL-2000; 2000US-216747P.
                                    09-AUG-2001
                                                                                                                                                     Human;
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                                                                                                                                                                                                                                                                                AAM84901 standard; Protein; 54 AA.
 17-JAN-2001; 2001WO-US01354
                                                                                                                                  cytostatic;
                                                                                                                                                                                  Human immune/haematopoietic antigen SEQ ID NO:12494.
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| 88 RSMTTGS 94
                                                                                                                                immune; haematopoietic; immune/haematopoietic antigen;
atic; gene therapy; vaccine; metastasis.
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ve J, Zhang Y,
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pred. No. 2.8;
9; Mismatches
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, Carter D;
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   28-JUN-2000;
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114 - SEP 2000;

21 - SEP 2000;

21 - SEP 2000;

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2000US-0180628.
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08-NOV
            WPI; 2001-483426/52
N-PSDB; AAK57682.
                             Rosen CA,
                                                              08-DEC
Nucleic acids encoding human immune/hematopoietic antigen polypeptides
                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                        17-NOV-2000;
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                            Barash SC,
                                                  2000US-0251990.
2000US-0254097.
2001US-0259678.
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                                                                                                                                                                     amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC complement the patients own production of (I). Additionally, (I) CC concers may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and treat immune/haematopoietic related diseases, especially CC cancers and cancer metastases of haematopoietic acityen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                                                     Query Match
Best Local
                                                                                 Matches
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                                                                                                                                                                     Sequence
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                          7 GQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPR----SGSTG
                                                                                                       Similarity
GOKGPVLWKPAHSPKDGHL-----GGPEL--EDPQPRLPLGTGAQG 39
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Search completed: June 17, 2003, 11:56:00 Job time: 15.1332 secs

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Result
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US-08-123-708-4

US-09-123-708-4

US-09-123-624-4

US-08-880-342-21

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US-09-066-074-2

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US-08-555-912A-2

US-08-804-4

US-09-208-804-4

US-08-801-743-4

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ZIP: 60064-3500
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CITY: Abbott Park
STATE: IL
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53.5 20.6 284 2 US-08-751-233A-6 Sequence 6, Appli 53 20.4 454 1 US-08-166-313-2 Sequence 2, Appli 53 20.4 574 2 US-08-966-713-2 Sequence 2, Appli 52.5 20.2 284 2 US-08-961-713-2 Sequence 8, Appli 52.5 20.2 1284 2 US-08-971-233A-8 Sequence 9, Appli 52.5 20.2 1284 2 US-09-343-494-9 Sequence 3336, Appli 51 19.6 485 2 US-09-134-001C-3336 Sequence 2, Appli 51 19.6 485 2 US-09-134-001C-3336 Sequence 2, Appli 51 19.6 485 2 US-09-390-200-2 Sequence 2, Appli 51 19.6 485 4 US-09-390-200-2 Sequence 2, Appli 51 19.6 485 4 US-09-390-200-2 Sequence 2, Appli 50.5 19.4 466 4 US-09-522-217-89 Sequence 2, Appli 50.5 19.4 466 4 US-08-868-435-2 Sequence 2, Appli 50.5 19.4 466 4 US-08-744-231-2 Sequence 2, Appli 50.5 19.4 466 4 US-08-785-31-2 Sequence 2, Appli 50.5 19.4 30.3 US-08-851-843A-203 Sequence 203, Appli 50.5 19.2 330 4 US-08-951-843A-203 Sequence 203, Appli 50.5 19.2 330 4 US-08-964-050-203 Sequence 203, Appli 50.5 19.2 330 4 US-08-964-050-203 Sequence 203, Appli 50.5 19.2 330 4 US-08-964-050-203 Sequence 203, Appli 50.5 19.2 570 4 US-08-969-046-4 Sequence 2, Appli 50.5 19.2 570 4 US-08-969-046-4 Sequence 2, Appli 50.5 19.2 570 4 US-09-198-122-2	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
.6 284 2 US-08-751-233A-6 Sequence 6, Ap 4 541 US-08-166-316-2 Sequence 2, Ap 4 574 2 US-08-906-711-2 Sequence 2, Ap 2 284 2 US-08-751-233A-8 Sequence 39. Ap 2 284 2 US-09-343-494-9 Sequence 39. Ap 2 284 2 US-09-134-001C-3336 Sequence 39. Ap 2 285 4 US-09-190-200-2 Sequence 29. Ap 2 285 4 US-09-390-200-2 Sequence 29. Ap 2 285 4 US-09-390-200-2 Sequence 29. Ap 2 285 4 US-09-390-200-2 Sequence 29. Ap 3 285 4 US-09-744-231-2 Sequence 29. Ap 3 285 4 US-08-744-231-2 Sequence 29. Ap 3 285 4 US-08-745-23-785-3 Sequence 29. Ap 3 285 4 US-08-851-843A-203 Sequence 29. Ap 3 285 4 US-08-854-050-203 Sequence 203. Ap 3 285 4 US-08-854-050-203 Sequence 203. Ap 3 285 4 US-09-430-323-203 Sequence 203. Ap 3 285 570 4 US-08-954-050-203 Sequence 29. Ap 3 285 570 4	50	50	50	50	50	50	50.5	50.5	50.5	51	51	51	51	52.5	52.5	53	53	53.5
2 US-08-751-233A-6 1 US-08-166-316-2 2 US-08-906-713-2 2 US-08-906-713-2 2 Sequence 2, Ap 2 US-08-751-233A-8 3 US-09-134-001C-333 4 US-09-134-001C-3336 5 Sequence 3, Ap 4 US-09-134-001C-3336 5 Sequence 2, Ap 4 US-09-1390-200-2 6 US-09-390-200-2 7 Sequence 2, Ap 7 US-08-686-435-2 8 Sequence 2, Ap 8 US-08-851-843A-203 8 Sequence 2, Ap 9 US-08-974-549A-322 9 Sequence 203, Ap 1 US-08-974-549A-322 9 Sequence 203, Ap 1 US-08-974-549A-323 1 US-08-974-549A-323 1 US-08-974-549A-323 2 Sequence 203, Ap 2 US-08-974-649A-323 3 US-08-974-649A-323 4 US-08-969-046-4 5 US-09-198-122-2 5 Sequence 2, Ap 8 Sequence 203, Ap 9 US-08-974-549A-323 9 Sequence 203, Ap 9 US-08-974-649A-323 9 Sequence 203, Ap 9 US-08-974-649A-323 9 Sequence 203, Ap 9 US-08-984-050-203 9 Sequence 203, Ap 9 US-08-994-050-203 9 Sequence 2, Ap 9 US-08-994-050-203 9 Sequence 2, Ap 9 US-08-999-046-4	19.2	19.2	19.2	19.2	19.2	19.2	19.4	19.4	19.4	19.6	19.6	19.6	19.6	20.2	20.2	20.4	20.4	20.6
-08-751-233A-6 -08-16-316-2 -08-16-316-2 -08-906-713-2 -08-906-713-2 -08-906-713-2 -09-343-494-9 -09-134-001C-3336 -09-134-001C-3336 -09-134-001C-3336 -09-134-001C-3336 -09-134-001C-3336 -09-134-001C-3336 -09-134-001C-3336 -09-138-203 -09-138-203 -08-96-046-4 -09-198-122-2 -08-96-046-4 -08-96-0466-4 -08-96-0466-4 -09-198-122-2 -08-96-0466-4 -08-96-0466-4 -08-96-0466-4 -08-96-0466-4 -09-198-122-2 -08-96-0466-4 -09-198-122-2 -08-96-0466-4 -08-96-0466-4 -09-198-122-2	603	570	330	330	330	330	600	466	466	510	485	485	265	1284	284	574	454	284
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## ALIGNMENTS

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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/065,383
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,385
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Chervi
              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                            REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                     NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                         TELEFAX: 847/938-2623

    Application US/09065383
    6391543

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HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
49 amino acids
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STROUPE, STEPHEN D.
VENTION: REAGENTS AND METHODS USEFUL
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                                             ; MOLECULE TYPE: US-09-065-383-27
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               Query Match
Best Local Similarity
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STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: No. (
                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8.
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: STROUPE, TITLE OF INVENTION:
                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                           TOPOLOGY:
                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                         NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                   TELEFAX: 847/938-2623
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                                                                                                                     ENGTH:
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                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abbott Park
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                                                                                                                     518 amino acids
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COLPITTS, TRAC
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                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                            linear
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S, STEVEN C.
, MICHAEL R.
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JOHN C.
STEPHEN D.
REAGENTS AND METHODS USEFUL
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRACEY L.
                                                                                                                                                                                                                                                                                                      08/842,385
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Pred. No. 5.1e-30;
Score 260; DB 4;
Pred. No. 8.9e-29;
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            Length 518;
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                                                                                                                       ; OTHER INFORMATION: Human thymidylate synthase protein sequence; PUBLICATION INFORMATION: DATABASE ACCESSION NUMBER: D00596/GenBank US-09-347-878-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-230-637-34
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                                                                                                                                                                                                                   SEQ ID NO 30
LENGTH: 313
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                  sequence 30, Application US/09347878C Patent No. 6376210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 34
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                                                             Matches
                                                                                          Query Match
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                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. 6264958el Genes of TITLE OF INVENTION: Associated Herpesvirus FILE REFERENCE: 1107.78372
CURRENT APPLICATION NUMBER: US/09/230,637
CURRENT FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                           APPLICANT: YUAD, Chong TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES FILE REFERENCE: 25885-1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 62

NUMBER OF SEQ ID NOS: 62

PASTSEQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                           Local
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6264958
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11 PLPPAAQERDAEPRPPHPELQYLGQIQHILRCG---VRKDDRTGTGT
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16; Conservative
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                           2 PLGPRGQDSPLLQRPQH--LMDQGQMRHSFSAGPELLRQDKRPRSGS
                                                             l Similarity
16; Conser
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Nicholas, John
Hardwick, J. Marie
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                                                          Pred. No. 3.3;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56.5; DI
Pred. No. 3.3;
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                                                                                        Length 313;
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                                                             Indels
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; FEATURE:
; OTHER INFORMATION: Wild type human thymidylate synthase amino acid
; OTHER INFORMATION: sequence (Genbank Accession number NF001062)
US-09-367-007C-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-066-074-2
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LENGTH: 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hunter
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PRIOR FILING DATE: 1998-01-03
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/367,007C CURRENT FILING DATE: 1999-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: D5978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof
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           SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acid
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13-NOV-1995
FILING DATE: 11-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
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                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: La Jolla
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                            NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
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es 16; Conserv
                                                                                                                              REFERENCE/DOCKET NUMBER:
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Liu-Chen, Xinyue
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4225 Executive Square, Suite 1400
               163 amino acids
                                                                       619/678-5099
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                                                     ID NO: 2:
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                                                                                                                                                  RESULT 8
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                                                                                                     Sequence 4, Patent No. (
                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                     Matches
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                                                                                        GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                            NUMBER OF SEQUENCES: 4
                                                           APPLICANT: Au-Your TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                      , Application US/09208804 6030826
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Haile, Lisa A.

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E: Incyte Pharmaceuticals, 3174 Porter Drive
                                                           Au-Young, Janice
VENTION: NOVEL HUMAN PARVULIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                         163 amino acids
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ative Square, Suite 1400
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Pred. No. 1.8;
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CITY:

Palo Alto

COMPUTER READABLE FORM:

Diskette

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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                           ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J
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LENGTH: 163 amino acids
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                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                          APPLICATION NUMBER: UPFILING DATE: Herewith
                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                         STREET: 3174 POI
CITY: Palo Alto
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          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                           MEDIUM TYPE:
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CLONE: 1332710
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REGISTRATION NUMBER:
                                                                            APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc
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PF-0217 US
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US-09-369-364A-13
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US-08-801-743-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
CURRENT APPLICATION NUMBER: US/09/031,563A CURRENT FILING DATE: 1998-02-26 NUMBER OF SEQ ID NOS: 27 SEQ ID NO 7
                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                Sequence 7, Application US/09031563A Patent No. 6022708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13
LENGTH: 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13,
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                               APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: P1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 639161
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (468)
OTHER INFORMATION: )
NAME/KEY: MOD_RES
LOCATION: (521)
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NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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TITLE OF INVENTION:
FILE REFERENCE: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens ADAMTS-9 FEATURE:
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LIBRARY: GC.
CNE: 1332710
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                                                                                                                                                                                                                                                                                                                    l Similarity
14; Conserv
                                                                                                                                                                                                                                                                                   8 QDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGS 46
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VENTION: Nucleic Acids Encoding Zinc Metalloproteases
VCE: 26473/4007/10-30-00
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Pred. No. 1.8;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 55;
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; ORGANISM: Homo sapiens US-09-031-563-7

TYPE: PRT LENGTH: 647

Query Match

Local

21.0%;

DB 3;

Length 647;

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; LENGTH: 647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-277-7
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-031-563-5
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GENERAL INFORMATION:
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No. 6451977
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Best Local 9
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                                                                   Best Local Similarity Matches 15; Conserv
                                                                                                     Query Match
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                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Fused FILE REFERENCE: P1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Fused FILE REFERENCE: P1272R1P1
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APPLICANT: Arnon Rosenthal
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APPLICANT: Arnon Roshenthal
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 292
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15; Conserv
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                                3 LGPRGQDSPLL-QRPQHLMDQGQMRHSFSAGPELLRQDKR------PRSGST 47
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LAPKGNQSRILTQAYKRMAEEAMQKKHQNTGPALEQEDKTSKVAPGTAPLPRLGAT 347
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                                                                   Conservative
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26.8%; Pred. No. 15;
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11; Mismatches
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RESULT 14

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-277-5
Search completed: June 17, 2003, 12:03:41 Job time: 5.51977 secs
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US-09-031-563-27
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SEQ ID NO 27
LENGTH: 1055
                                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserv
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APPLICANT: Arnon Rosenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: P1272R1P1
CURRENT APPLICATION NUMBER: US/09/392,277A
CURRENT FILING DATE: 1999-09-03
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APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
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15; Conserv
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Pred. No. 15;
11; Mismatches
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Pred. No. 28;
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Minimum DB seq
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Perfect score:
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length: 2000000000
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Listing first 45 summaries
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Result

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Sequence 8, Appli	Sequence 1392, Ap	Sequence 2, Appli	Sequence 5, Appli	Sequence 12, Appl	Sequence 9, Appli	Sequence 32, Appl	Sequence 31, Appl	Sequence 8, Appli	Sequence 129, App	Sequence 125, App	Sequence 14, Appl	Sequence 10, Appl	Sequence 25, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 35805, A	Sequence 46074, A	Sequence 44434, A	Description

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52.5	52.5	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53	,
20.2	20.2	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	
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Sequence 11, Appl	Sequence 9, Appli	Sequence 51, Appl	Sequence 164, App	Sequence 4, Appli	Sequence 25, Appl	Sequence 164, App	Sequence 4, Appli	Sequence 25, Appl	Sequence 164, App	Sequence 5, Appli	Sequence 25, Appl	Sequence 164, App	164	Sequence 164, App	164	164			•	Sequence 164, App	Sequence 2, Appli	Séquence 5, Appli	Sequence 43, Appl	Sequence 43, Appl	Todac an annual

### ALIGNMENTS

Sequence 44434, Application US/09864761 Patent No. US20020048763A1

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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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APPLICANT: Rank,
APPLICANT: Hanze
                                                                       PRIOR FILING DATE: 2001-0: PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US01/00665
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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FILING DATE: 2001-01-29
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                  NUMBER: PCT/US01/00662
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Pred. No.
7; Mismatc
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BRAIN, SIGN
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Best Local :
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SEQ ID NO 46074
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN BRAII
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APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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Chen, Wensheng
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EXPRESSED IN PLACENTA, SIGNAL = 1.4
EXPRESSED IN BONE MARROW, SIGNAL = 2
EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
EXPRESSED IN LUNG, SIGNAL = 3.4
EXPRESSED IN LUNG, SIGNAL = 3.4
EXT_HUMAN HIT: BF314489.1, EVALUE 2.00e-28
SMISSPROT HIT: Q13526, EVALUE 2.00e-29
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5.5;
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PCT/US01/00663

FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30

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RESULT 5
US-09-918-171A-13
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Patent No. US20020090373A1
GENERAL INFORMATION:
APPLICANT: PFIZER INC.
                                                                                                                                                                                                          Best
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                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/972,467
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: PC10850A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BH410, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
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                                                                                                                                                                                                          Local Similarity
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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                                                                                      1288 QDCSMSPCPQRTPDSGLAQHPFQ----NEDYRPRSAS 1320
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71.4%;
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Pred. No. 3;
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RESULT 7

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: LOCATION: (521)
: OTHER INFORMATION: Xaa = Tyr
US-09-918-171A-13
                                                                                                                                                     ; ORGANISM: homo sapiens US-09-938-330-25
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US-09-938-330-25
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                                                                                                             Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020115838A1el Human Proteases and Polynucleotides Enco
FILE REFERENCE: LEX-0237-USA
CURRENT APPLICATION NUMBER: US/09/938,330
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirobata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/04193
CURRENT APPLICATION NUMBER: US/09/918,171A
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Scoville, Johr
APPLICANT: Friddle, Carl
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NUMBER OF SEQ ID NOS: 31
SOFTWARE. PARTIES
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                                                                                                                                                                                            TYPE: PRT
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LOCATION: (468)
OTHER INFORMATION:
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es 14; Conserv
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1260 QDCSMSPCPQRTPDSGLAQHPFQ-----NEDYRPRSAS 1292
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                                 8 QDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGS 46
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Pred. No. 3.2e+02;
3; Mismatches 16
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Pred. No. 3.1e+02;
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US-10-224-249-14; Sequence 14, Application US/10224249; Publication No. US20030087867A1; GENERAL INFORMATION:
                   RESULT 9
US-10-108-605-125
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LENGTH: 1315
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Sequence 125,
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SEQ ID NO 14
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Verlinden, Stefan F.F.

TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis FILE REFERENCE: 2183-523US
CURRENT APPLICATION NUMBER: US/10/224,249
CURRENT FILING DATE: 2002-08-19
FRIOR APPLICATION UMBER: PCT/NL00/00482
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: EP 99202263.2
PRIOR APPLICATION NUMBER: EP 99202263.2
PRIOR FILING DATE: 1399-07-09
PRIOR FILING DATE: 1399-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/143,101 PRIOR FILING DATE: 1999-07-09 NUMBER OF SEQ ID NOS: 16
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APPLICANT: Carpenter, David A.
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CHAIN
LOCATION: (1)..(1433)
OTHER INFORMATION: Human nitric oxide synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                   124 QPLGPPTKAVDLSHQPPAGKEQPLAVDGASGPGNGPQHAYDDGQEAGSLPHANGWPQAPR 183
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15; Conserv
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Application US/10108605
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Pred. No. 2.4e+02;
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Pred. No. 2.7e+02;
5; Mismatches 16;
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RESULT 11
US-10-059-585-8
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US-10-108-605-129
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US-10-108-605-129
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SEQ ID NO 129
LENGTH: 623
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Best Local
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Patent INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/176,418 PRIOR FILING DATE: 2000-01-14 NUMBER OF SEQ ID NOS: 361
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PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODTITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOFFILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
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TYPE: PRT
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Local Similarity 35.4%;
nes 17; Conservative
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nes 17; Conserva
                                                                              110 QQSLLLQHPQQQQQQHSHQSQQQQQQHGYGSSAQL--PHHRLSGGSTGS 155
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US20020160934A1
                                                                                                                       QDSPLLQRPQHL-----MDQGQMRHSFSAGPELLRQDKRPRSGSTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bachmann,
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                                                                                                                                                                Conservative
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Pred. No. 1.2e+02;
                                                                                                                                                                                   Score 54; DB 9;
Pred. No. 1.2e+02;
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Sequence 8, Application US/10059585 Publication No. US20030082776A1

GENERAL INFORMATION:

APPLICANT: Ota, Toshio

APPLICANT:

Nishikawa,

Tetsuo

Takao

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US-08-817-832B-31; Sequence 31, Application US/08817832B; Publication No. US20030104516A1;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/JP00/05060 PRIOR FILING DATE: 2000-07-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/183,322 PRIOR FILING DATE: 2000-02-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN TILE OF INVENTION: KINASE/PROTEIN PHOSPHATASE TLE REFERENCE: 06501-098001
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                                                                                                                                                                                               STREET: 225
CITY: Chicago
CITY: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 638
                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
               FILING DATE: 28-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                     APPLICATION NUMBER:
 APPLICATION NUMBER:
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FILING DATE: 2000-01-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LQRPQHL-----MDQGQMRHSFSAGPEL---LRQDKRPRSGSTGS 49
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                                                                                                                                                                                                                                                  E: Marshall, O'Toole, Gerstein, Murray & Borun
233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamatsu, Ai
Nagai, Keiichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nezu, Jun-Ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Funahashi, Shin-Ichi
                                                                                                                                                                                                                                                                                                                            MANDELKOW, Eckhard, et al.
VENTION: No. US20030104516A1el Protein Kinase (NPK-110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                   28-APR-1997
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WO PCT/EP95/04258
                                                     US/08/817,832E
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                                                                                                                    RESULT 14
US-10-142-356-9
                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORWATION: GenBank Accession No: US20030087317A1 g2052189
; DATABASE EMTRY DATE: 25 April 1997
US-10-195-101-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-817-832B-31
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                                                               Sequence 9, Application US/10142356 Publication No. US20030036183A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PERL Program
SEQ ID NO 32
LENGTH: 793
TYPE: PRT
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Best Local Similarity
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APPLICANT: Bowers, Alex J.
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FILE REFERENCE: 01017/37177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/19:
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 09/523,849
PRIOR FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
                                   APPLICANT: Boylan, John F. APPLICANT: Bowers, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hodgson, David M.
TITLE OF INVENTION: HUMAN NIM1 KINASE
FILE REFERENCE: PC-0009-1 CIP
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rattus norvegicus
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APPLICATION NUMBER:
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les 17; Conserv
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amino acid
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Bosotti, Roberta
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Isacchi, Antonella
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36.2%;
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Pred. No. 1
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Pred. No. 1.5e+02
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CURRENT APPLICATION NUMBER: US/10/142,356
CURRENT FILING DATE: 2002-05-09

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PRIOR APPLICATION NUMBER: 60/290,276

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARRE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-356-9
                                                                                                                                                                                                                 APPLICANT: Feng, Jia-Jia
APPLICANT: Reinhard, Christoph
APPLICANT: Fentl, Wendy J.
APPLICANT: Fantl, Wendy J.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING PAR-1
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYNUCLEOTIDES AND METHODS UTILIZI
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: PP-016093.002/200130.525
CURRENT ETLING DATE: 2001-07-30
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 795
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-919-585-12
Sequence 12, Application US/09919585
Patent No. US20020115167A1
Search completed: June 17, 2003, 12:02:32 
Job time: 6.23719 secs
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APPLICANT: Feng, Jia-Jia
APPLICANT: Reinhard, Chri
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5; Mismatches 15; Indels 10;
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#### ALIGNMENTS

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R.Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Evol. 38, 637-641, 1994
A;Title: Drive-selection equilibrium: homopolymer evolution
A;Reference number: Z17850; MUID:94365848; PMID:8083889
A;Accession: T1398
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1655 SNEW
                                                                                                                                                                                                                                                                                  gene mastermind protein - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: PA5166
C;Superfamily: nitrogen assimilation regulatory protein ntrC; response
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A;Accession: G83000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <STO>
A;Cross-references: GB:AE004929; GB:AE004091; NID:g9951462; PIDN:AAG08551.1;
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                          A;Cross-references: FlyBase:FBgn0013119
                                                                                                                A;Cross-references: EMBL:M92914; NID:g157833; PID:g157834; PIDN:AAC37201.1
Query Match
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; U.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A; Residues: 1-345 <KAW>
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein APE1577 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72536
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A; Experimental source: strain R1
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A; Residues: 1-333 <WHI>
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A;Experimental source: strain Kl
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                                                                                      WPSPTRKRGGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.; Hino, Y.;
   Hex
                                                                                                                                                                                        ----PRGQDSPLLQRPQHLMDQ-----GQM----RHSFSAGPEL----LR
                                                                                                                                                                                                                                          22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikawa, H.; Ya
, S.; Funahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 2
Pred. No. 5.9;
7; Mismatches
                                                                                                                                                                                                                        Score 59.5; DB Pred. No. 7.1; 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE000513; NID:g6459742; PIDN:AAF11509.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamazaki, S.; Haikawa, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.; Tanaka, T.;
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                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Peterson, J.D.; Dodson, Utterback, T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kudoh,
                                                                                                                                                                                                                          25;
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    Y.; Jin-no,
    Y.; Yamaza

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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-276 < PEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S54830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-271 <BED>
                                                   A; Introns: 29/3;
                                                                 A; Map position:
                                                                                                                                                                                                        A; Reference number: A; Accession: T13853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                     A; Cross-references:
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-3429 <
                                                                                                                                                                                          A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                      Genetics:
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Best Local
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19; Conserv
Similarity
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 22.5%;
41.0%;
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Pl protein - potato virus Y (fragment)
C;Species: potato virus Y, PVY
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Nov-2000
C;Accession: S54830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regu F;139-195/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 21, 1245-1249, 1993
A;Title: HEX: a novel homeobox gene expressed during haematopoiesis
A;Reference number: S30230; MUID:93219088; PMID:8096636
                                                                                                                                                                                                                                                                                                                                                          C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C;Accession: T13853
                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein X - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: Potato plants transformed with a potato A; Reference number: {\tt S54830}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S54830
R;Pehu, T.; Maki-Valkama, T.; Valkonen, J.P.T.; Koivu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Bedford, F.K.; Ashworth, A.; Enver, T.; Nucleic Acids Res. 21, 1245-1249, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                           A; Description: A novel gene, A; Reference number: 217797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X82848; NID:g817817; PIDN:CAA58051.1; PID:g817818
                                               A; Cross-references: FlyBase: FBgn0023458
                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPLGPRG--QDSPLLQ----RPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tobacco etch virus
  102/2; 152/1; 2478/1; 2838/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                               EMBL: X97196; NID: g1279383; PID: e236567; PIDN: CAA65830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: Z21524; NID: g288500; PIDN: CAA79729.1; PID: g288501
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45.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome polyprotein
                                                                                                                                                                                                                                                                                April 1996
on the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2;
  2913/1;
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                                                                                                                                                                                                                                                                                                                                                                                  #text_change, 17-Nov-2000
                                                                                                                                                                                                                                                                                      X-chromosome;
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3032/1; 3120/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus Y P1
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                                                                                                                                                                                                                                                                                   a homologue
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  3149/3; 3239/3
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Score 58.5; Pred. No. 1.

DB 2;

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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
                                                                                                                                              transcription regulator, LacI family [imported] - Caulobacter crescentus C:Species: Caulobacter crescentus C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
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H87433
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A: Residues: 136-195 <BEW>
A: Cross-references: EMBL::
C: Comment: This protein i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Bedford, F.K.
submitted to the EMBL Data
submitted to the EMBL Data
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                Proc. Natl. Acad. Sci. U.
A; Title: Complete Genome
                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:L16499; NID:g292404; PIDN:AAA02988.1; PID:g292405 R;Crompton, M.R.; Bartlett, T.J.; MacGregor, A.D.; Manfioletti, G.; Buratti, Nucleic Acids Res. 20, 5661-5667, 1992 A;Title: Identification of a novel vertebrate homeobox gene expressed in haer A;Reference number: S26799; MUID:93087175; PMID:1360645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A: Residues: 1-270 <ACC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;138-194/Domain: homeobox homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
A;Reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nomeobox protein HEX - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: unassigned homeobox proteins; Keywords: DNA binding; homeobox; nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-114,'L',116-270 <CRO>
Cross-references: EMBL:X67235; NI
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type: DNA
: 122-270 <BED>
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                                                                                                                              H87433
                                                                                                                                                                                                                                                                                                       DPLGKPLLWSPFLQRPLHKRKGGQVRFS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSRLLAKKQRL---NQVLHTFAHDPE----SRSPRSGET 1365
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A87249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        important regulator of
                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB
Pred. No. 8.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            2
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                  lobacter crescentus.
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A; Map position:
C; Superfamily:
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C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Goodner, B.; Hinkle, G.; G;
A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
                                                                                          C; Genetics:
                                                                                                                                                                                                    A; Reference number: A; Accession: AD2784
                                                                                                                                                                                                                     A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                       A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; ster, E.W.
                                                                                                                                                                                                                                                                                         R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                             C; Accession: AD2784
                                                                                                                                                                                                                                                                                                                                                                                C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                   molybdopterin biosynthesis protein [imported] - Agrobacterium; tumefaciens C; Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome Sequence of the Plant Pathogen and A;Reference number: A97359; PMID:11743194 A;Accession: D97563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AGR_C_3105 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-C;Accession: D97563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-357 <STO>
A;Cross-references: GB:AE005673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: p
A;Molecule
                                                                                                         A;Cross-references: GB:AE008688; PIDN:AAL42690.1; A;Experimental source: strain C58 (Dupont)
                                                                                                                                                 A; Residues:
                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                 A:Status: preliminary
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A; Residues: 1-405 < KUR>
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                                                        position:
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15; Conserv
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                                     molybdenum cofactor biosynthesis protein moeA-2
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C.; Allinger,
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   57.5;
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                                                                                                                              GSPDB:GN00186
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Markelz,
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A; Gene:
C; Superf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 2-27;95-101;131-155;159-169;188-195;245-263;297-302;340-350;383-388;407-419;
A; Residues: 7-27;95-101;131-155;159-169;188-195;245-263;297-302;340-350;383-388;407-419;
R; Dierks, T; Miech, C; Hummerjohann, J;; Schmidt, B; Kertesz, M.A.; von Figura, K.
J. Biol. Chem. 273, 25560-25564, 1998
A;Title: Posttranslational formation of formylglycine in prokaryotic sulfatases by modification
A; Rote enumber: A59074; MUID:98421466; PMID:9748219
A; Rote enumber: A59074; MUID:98421466; PMID:9748219
A; Rote: confirmation of 3-oxoalanine active site, referred to as formylglycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Blochem. 229, 385-394, 1995
A;Title: Purification and characterization of the arylsulfatase
A;Reference number: S69336; MUID:95262702; PMID:7744061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 17-Jul-1998 #sequence_revision
                                                                                                                                                                   A;Cross-references: GB:AE004456; GB:AE004091; NID:g9946013; PIDN:AAG03573.1; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Beil, S.; Kehrli, H.;
Eur. J. Biochem. 229, 31
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-536 <STO>
                                                                                                                                                                                                                                                                         A;Reference number: A82950;
A;Accession: D83622
                                                                                                                                                                                                                                                                                                                                                                                                   R;Stover, C.K.; Pham, X.Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arylsulfatase PA0183 [imported] - Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Species: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:Z48540; NID:g2440146; PIDN:CAA88421.1; Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                Title: Complete genome
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                                           Similarity
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50; MUID:20437337; PMID:10984043
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L.L.;
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                                         Score 57;
Pred. No.
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                     Mismatches
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Larbig,
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K.; Lim,
                                                                                                                                                                                                                                                                                                                patho
                   RESULT 15
D86350
                                                                                                                                                                                                                                                                                      A;Cross references: GDB:120465; OMIM:188350
A;Map position: 18p11.32-18p11.32
A;Introns: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3
C;Superfamily: thymidylate synthase; thymidylate synthase homology C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase F;30-313/Domain: thymidylate synthase homology <TDS>
                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Davisson, V.J.; Sirawaraporn, W.; Santi, D.V. J. Biol. Chem. 264, 9145-9148, 1989
A; Title: Expression of human thymidylate syntha A; Reference number: A33842; MUID:89255401; PMID A; Accession: A33842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Structural and Functional Analysis of the Human Thymidylate Synthase A;Reference number: 155318; MUID:91056070; PMID:2243092 A;Accession: 155318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A23047; I55318; JU0120; A22393; A33842 R;Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, Nucleic Acids Res. 13, 2035-2043, 1985 A;Title: Nucleotide sequence of a functional cDNA for human A;Reference number: A23047; MUID:85215597; PMID:2987839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-313 < RES>
                                                                                                                                                                                                                                                                       F;199/Active site: Cys
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: TYMS
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A; Residues: 1-68 <TA2>
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F8K7.13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Shimizu, K.; Ayusawa, D.; Ta
J. Biochem. 97, 845-850, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X02308; NID:g37478; Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Biol. Chem. 265, 20277-20284, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Homo sapiens (man)
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protein
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16; Conser
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                                                                                                                                             PLGPRGQDSPLLQRPQH--LMDQGQMRHSFSAGPELLRQDKRPRSGS
                                                                                                    PLPPAAQERDAEPRPPHGELQYLGQIQHILRCG--
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Arabidopsis
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1989
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    thaliana
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Pred. No. 15;
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7; Mismatches
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PMID:3839505
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Shimizu, K.; Gotç
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
Search completed: June 17, 2003, 12:01:16 Job time: 7.86764 secs
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C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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A;Molecule type: DNA
A;Residues: 1-807 <STO>
A;Cross-references: GB:AEO05172; NID:g5263321; PIDN:AAD41423.1; GSPDB:GN00141
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Best Local Similarity 29.6
Matches 16; Conservative
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Pred. No. 44;
7; Mismatches 22;
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RL18_YEAST
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PINI_MOUSE
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DL1.3_HCMVA
PNT1_DARME
CCAA_RAT
CLH1_HUMAN
CLH_RAT
POLG_PVYN
4CL3_ARATH
RGS9_RAT
MI.46_HUMAN
ICAL_SHEEP
POLG_PYB_POLG_PYBB_PSEPUU
RGS9_MOUSE
PYBB_PSEPUU
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8 homo sapien
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         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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52         20.0         704         1 SYN1_RAT         P09951 rattus norv           52         20.0         706         1 SYN1_BOYIN         P1759 bos taurus           52         20.0         809         1 PBPA_XYLFA         O9p9d4 xylella fas           51.5         19.8         1640         1 CLH2_HUMAN         P53675 homo sapien           51.5         19.8         275         1 VINT_FRG3V         P29164 frog virus           51.5         19.8         275         1 VINT_FRG3V         P29164 frog virus           51.5         19.8         275         1 VINT_FRG3V         P7658 escherichia           51.5         19.8         2832         1 NDVB_RHIME         P20471 rhizobium m           51.5         19.6         346         1 MGB4_HUMAN         015481 homo sapien           51         19.6         501         1 VMAO_YERST         015488 homo sapien           51         19.6         501         1 VMAO_YERST         023212 saccharcomyc           51         19.6         839         1 VPP1_MOUSE         0292194 mus musculu
704 1 SYN1_RAT P09951 706 1 SYN1_BOYIN P17599 809 1 PBPA_XYLFA QPpdd 1640 1 CLH2_HUMAN P53675 1 VINT_FRG3V P29164 759 1 MAO2_ECOLI P76558 2832 1 NIVB_RHIME P20471 346 1 MGB4_HUMAN P54814 550 1 YM40_YEMST Q03212 839 1 VPP1_MOUSE Q92144
1 SYN1_RAT P09951 1 SYN1_BOVIN P17599 1 PBPA_XYLFA OPPG40 1 CLH2_HUMAN P53675 1 2SS3_ARATH P15459 1 VINT_FRG3V P291640 1 MAO2_ECOLI P76558 1 NDVB_RHIME P20471 1 MGB4_HUMAN O15481 1 YM40_YEAST O15481 1 YM40_YEAST Q9z144
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rattus norv bos taurus xylella fas homo sapien arabidopsis frog virus escherichia rhizobium m homo sapien homo sapien saccharomyc mus musculu

## ALIGNMENTS

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1683	HUMAN HXB9_HUI
	15-JUN-2002 (Rel. 41, Last sequence update)
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	Obordutu. Orumiutu. Vortobrutu.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
٠.	ROM N.A.
	KOsaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;
	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
•	SEQUENCE FROM N.A.
	TISSUE=Muscle;
	Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. > '
_	OF 173-250 FBOK N
	TISSUE-Placenta;
	MEDLINE-89378558; PubMed-2570724;
	D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G.,
_	Simeone A., Boncinelli E., Peschle C.;
-	Dosterior axis in embryonic central nervous system.":
•	ferentiation 40:191-197(1989).
_	[4]
	MEDLINE=90215256; PubMed=2576652;
	., Acampora D., Pannese M., D'Esposito M., Somma
	<pre>M., Faiella A., Simeone i bbox genes.";</pre>
	Genome 31:745-756(1989).
	-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
	SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
``	
	<ul><li>-!- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT 5-9 WEEKS FROM CONCEPTION.</li></ul>
	!- SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMI
• ` `	This SWISS-DEOT betry is conveight. It is produced through a collaboration
	between the Swiss Institute of Bioinformatics and the EMBL outstation -
	the European Bioinformatics Institute. There are no restrictions on its

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                                                                   This SWISS-PROT entry is copyright. It is produced through a copyright that is produced through a copyright the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institute. There are no restrict is by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P02833; 9ANT
TRANSFAC; T01738; -
Genew; HGNC:5120; HOXB9
                                                                                                                                                                                                                                                                      Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Q92794;
          MIM; 601408;
                   Genew;
                          EMBL; U47742;
                                            or send an email to license@isb-sib.ch).
                                                     entities requires a
                                                              modified and this statement
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96376968; PubMed=8782817;
                                                                                                                                                                                                                                                                                              Monocytic leukemia
ZNF220 OR MOZ.
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DNA_BIND 185 244
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                 HGNC:13013;
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IPR001386; Histone_H1/H5
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AAG42144.1;
AAH15565.1;
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F06ECBC08FBBED2C CRC64;
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STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-93219088; PubMed-8096636;
MEDLINE-93219088; PubMed-807678;
MEDLINE-93219088; PubMed-807688;
MEDLINE-93219088; PubMed-807688;
MEDLINE-100888;
MEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by arentities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                              conserved between mouse and human.";
nucleic Acids Res. 21:1245-1249(1993).
-i-FUNCTION: RECOGNIZES THE DNA SEQUENCE 5'-ATTAA-3'.
IN HEMATOPOIETIC DIFFERENTIATION.
                                                                                                                                                                                                                                                                                       Bedford F.K., Ashworth A., Enver T., v"HEX: a novel homeobox gene expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHEX OR PRHX.
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Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
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InterPro; IPR001965; Znf_PHD
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMUJJD; .... PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Developmental protein;
HOMEOBOX; DNA-binding; Developmental protein;
                                                                                       Bedford F.K., Ashworth A., L....
Bedford F.K., Ashworth A., L....
"HEX: a novel homeobox gene expressed
"HEX: a novel homeobox gene expressed
"A horiveen mouse and human."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMPH_HUMAN
Q03014;
                                      Nucleic Acids Res. 21:1243-1243(15)
[5]
3D-STRUCTURE MODELING OF 136-196.
MEDLINE=94259190; PubMed=7911091;
                                                                                                                                                                                                                              Hromas R.A., Collins S.J., Radich J.;

"PCR cloning of an orphan homeobox gene (PRH) preferentially expressed in myeloid and liver cells.";

Biochem. Biophys. Res. Commun. 195:976-983(1993).
                                                                                                                                                                                                                                                                                                                              Crompton M.R., Bartlett T.J., Macgregor A.D., Manfioletti
Buratti E., Giancotti V., Goodwin G.H.;
"Identification of a novel vertebrate homeobox gene expres
haematopoietic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29,
01-JUN-1994 (Rel. 29,
15-JUN-2002 (Rel. 41,
                                                                                                                                   MEDLINE-93219088;
                                                                                                                                              SEQUENCE OF 122-270 FROM N.A.
                                                                                                                                                                                  TISSUE=Bone marrow;
Strausberg R.;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=93384629;
                                                                                                                                                                                                                                                                                                                    Nucleic
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-93087175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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          protein Prh,
         "A homology-based molecular model of the proline-rich homeodomain protein Prh, from haematopoietic cells.";
                                  Neidle S., Goodwin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR PRHX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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                                                                                                                                                                                                                                                                                                                    Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPEL
                                                                                  between mouse and human.";
cids Res. 21:1245-1249(1993).
                                                                                                                                                                     (OCT-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR PRH OR HEX.
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                                                                                                                                PubMed=8096636;
                                                                                                                                                                                                                                                                                PubMed=8103988;
                                                                                                                                                                                                                                                                                                                                                                              PubMed=1360645;
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45.78;
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, Last annotation update)
(Hematopoietically expre
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Pred. No.
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Pred. No. 4.1
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Catarrhini; Hominidae
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                                                                                                                     Wiedemann
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                            NFC1_HUMAN STANDARD: PRT: 943 AA. 095644; Q12865; Q15793; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Nuclear factor of activated T-cells, cytoplasmic complex cytosolic component) (NF-ATC1) (NF-ATC). NFATC1 OR NFATC OR NFATC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                       TISSUE-B-cell
                                            SEQUENCE FROM
                                                                                                                 T-cell
                                                                                                                                                         MEDLINE-94261186; PubMed-8202141;
Northrop J.P., Ho S.N., Chen L., Th
Nolan G.P., Admon A., Crabtree G.R.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                         Nature 369:497-502(1994).
                                                                                                                                                       Nolan G.P., Admon
                                                                                                                                                                                                                              TISSUE-T-cell,
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox;
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                                                                                                                                  NF-AT components
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SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: LIVER AND PROMYELOCYTIC LEUKEMIA CELL
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and Peripheral blood lymphocytes.
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Pred. No. 5.4;
2; Mismatches 1
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9C16BB6D494475FC
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                                                                                                                                      of transcription
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T-IXMPHOCYTES AS WELL AS IXMPHOID AND MONIXMPHOLOGIAN OF THE MULTICOMPONENT AND MONIXMPHOLOGIALS.

T-IXMPHOCYTES AS WELL AS IXMPHOID AND MONIXMPHOID CELLS.

THAT CONSISTS OF AT LEAST TWO COMPONENTS, A PRE-EXISTING CYTOPLASMIC COMPONENT NEATC 2 AND AN INDUCIBLE NUCLEAR COMPONENT NEATC1. OTHER MEMBERS SUCH AS NEATC4, NEATC3 OR MEMBERS OF THE COMPLEX. NEATC PROTEINS BIND TO DNA AS MOOMERS.

THE COMPLEX. NEATC PROTEINS BIND TO DNA AS MOOMERS.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC FOR THE PHOSPHORYLATED FORM AND NUCLEAR EXIT OF NEATC IS THOUGHT TO BE ONE MECHANISM BY WHICH CELLS DISTINGUISH BETWEEN SUSTAINED AND TRANSIENT CALCIUM SIGNALS. THE SUBCELLULAR LOCALIZATION OF NEATC PLAY A KEY ROLE IN THE GENE TRANSCRIPTION.

ALPHA, B-BETA, C-ALPHA (SHOWN HERE) AND C-BETA; ARE PRODUCED BY ALTERNATIVE PRODUCES: AT LEAST 6 ISOFORMS; A ALPHA, A-BETA, B-ALPHA, B-BETA, C-ALPHA (SHOWN HERE) AND TIONAL ISOFORMS PRODUCED BY ALTERNATIVE INITIATION AT MET-37 OF ISOFORMS ALPHA. NEATC/C IS THE STRONGEST ACTIVATOR OF GENE TRANSCRIPTION, FOLLOWED BY ALTERNATIVE INITIATION AT MET-37 OF ISOFORMS ALPHA. NEATC/C. BOTH PRESENT IN T-CELLS CAN MODULATE THEIR TRANSCRIPTIONAL ACTIVITY.

-1- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, PERLIPHERAL LEUKOCYTES AS T-CELLS (THYMUS AND PERLIPHERAL LEUKOCYTES AS NEATC/B AND NEATC/C ARE PREFERENTIALLY EXPRESSED IN NATUE T-CELLS (STRUBE EXPRESSED IN NAIVE T-CELLS AFTER FIRST ANTIGEN EXPOSURE AND ISOFORM A IS EXPRESSED IN NAIVE T-CELLS AFTER FIRST ANTIGEN EXPOSURE AND ISOFORM A IS EXPRESSED IN EFFECTOR T-CELLS AFTER EXPOSURE AND EXPOSURE AND ISOFORM A IS EXPRESSED IN EFFECTOR T-CELLS
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"Generic signals and calcineurin, and NF-A Cell 96:611-614(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20119316; PubMed-10652349;
Porter C.M., Havens M.A., Clipstone N.A.;
"Identification of amino acid residues and protein kinases involved the regulation of NFATC subcellular localization.";
J. Biol. Chem. 275:3543-3551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brabletz T., Serfling E.; "Multiple NF-ATC isoforms with individual transcriptional properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chuvpilo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fischer C., Inashkina I. Schmitt E., Serfling E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99189746; PubMed=10089876
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Kerstan A., Escher C.,
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"Characterization of a new isoform of
activated T cells) gene family member
J. Biol. Chem. 271:20914-20921(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW
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MEDLINE-99170294; PubMed-10072078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-B-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PLAYS A ROLE IN THE INDUCIBLE EXPRESSION OF CYTOKIN GENES IN T CELLS, ESPECIALLY IN THE INDUCTION OF THE IL-2 OR GENE TRANSCRIPTION. ALSO CONTROL GENE EXPRESSION IN EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARDIAC CELLS. COULD REGULATE NOT ONLY THE ACTIVATION AND PROLIFERATION BUT ALSO THE DIFFERENTIATION AND PROGRAMMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takeuchi A., Sharma S.;
Chem. 271:33705-33705(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ized in T lymphocytes.";
162:7294-7301(1999).
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Inashkina I., Jankevics E., Berberich-Siebelt F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and specific outcomes: signaling through Ca2+.
NF-AT.";
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EXPOSURE
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IL-2 OR IL-4
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--- IDOMAIN: REL SIMILARITY DOMAIN (RSD) ALLOWS DNA-BINDING AND COOPERATIVE INTERACTIONS WITH API FACTORS
--- I-- DOMAIN: THE N-TERMINAL TRANSACTIVATION DOMAIN (TAD-A) BINDS TO AND IS ACTIVATED BY CBB/P300. THE DEPHOSPHORYLATED FORM CONTAINS TWO UNMASKED NUCLEAR LOCALIZATION SIGNALE (NLS), WHICH ALLOW TRANSLOCATION OF THE PROTEIN TO THE NUCLEUS.
--- I-- DOMAIN: NEATC/C HAS A C-TERMINAL PART WITH AN ADDITIONAL TRANSACTIVATION DOMAIN, TAD-B, WHICH ACTS AS A TRANSCRIPTIONAL PART WITHOUT COMPLETE TAD-B WHICH ACTS AS A TRANSCRIPTIONAL REPRESSOR.

--- PTM: PHOSPHORYLATED BY NEATC-KINASE; DEPHOSPHORYLATED BY
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EMBL; U08015; # EMBL; U59736; # EMBL; U80917; # EMBL; U80918; # MUTAGEN MUTAGEN Pfam; PF00554; RHD; 1. Pfam; PF01833; TIG; 1. MUTAGEN VARSPLIC VARSPLIC VARSPLIC VARSPLIC DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN Transcription DNA-binding; ! PROSITE; SMART; SM00429; IPT; InterPro; IPR002909; IPT\_TIG.
InterPro; IPR000451; NF\_Rel\_dor\_fam. MIM; 600489; Genew; HGNC:7775; NFATC1. TRANSFAC; EMBL; U80919; DOMAIN REPEAT REPEAT REPEAT DOMAIN DOMAIN PS01204; REL\_1; PS50254; REL\_2; T01945; 169 869 717 Alternative AAA19601.1; -.; AAC50869.1; -.; AAD00450.1; -.; AAD00451.1; -.; AAD00452.1; -.; regulation; 169 943 943 716 splicing; Phosphorylation; Repeat.
CALCINEURIN-BINDING.
TRANS-ACTIVATION DOMAIN A (TAD-A) FALSE\_NEG Activator; LOCALIZATION.
S->A: PARTIAL
S->A: NO EFFEC A-BETA). MISSING (IN MPSTSFPVPSKFPLGPAAAVFGRGETLGPAPRAGGTMKSAE E -> MTGLEDQEFDFEFLFEFNQRDEGAAAAAP (IN ISOFORM A-BETA, ISOFORM B-BETA AND B-BETA). S->A: NO EFFECT ON SUBCELLULAR MISSING (IN VPIIKTEPTDDYEPAPTCG PHOSPHORYLATION. TRANS-ACTIVATION DOMAIN B (TAD-B). NUCLEAR EXPORT SIGNAL. NUCLEAR LOCALIZATION SIGNAL DNA-BINDING NUCLEAR LOCALIZATION SIGNAL. ISOFORM C-BETA) SP REPEATS PARTIAL NUCLEAR TRANSLOCATION NO EFFECT ON SUBCELLULAR ISOFORM Repressor; Nuclear protein; ISOFORM B-ALPHA AND ISOFORM A-ALPHA AND ISOFORM A-ALPHA AND Ÿ GNAIFLTVSREHERVGCF ISOFORM

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Mammalia; Eutheria;
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                                                                                                                                            SMART; SM00389; HOX; 1.
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that of hepatocyte nuclear factor-6.";
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16-0CT-2001
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                                                                                                                                                                                                                                    EMBL; Y18198; CAB38253.1;
                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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MEDLINE-99115605; PubMed-9915796;
                                                                                                                                                                                                                          TRANSFAC; T03259;
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                                                                                                                                                                                                                                                                                                                                                                                                           Jacquemin P., Lannoy V., Rousseau G.G., Lemaigre F.P., "OC-2, a novel mammalian member of the ONECUT class of transcription factors whose function in liver partial)
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                                                                                                    Activator.
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                                                                                                                                                                               InterPro; IPR003350; Hmoeo_CUTInterPro; IPR001356; Homeobox.
                                                                                                             ranscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                  3101. Chem. 274:2665-2671(1999).
FUNCTION: TRANSCRIPTIONAL ACTIVATOR. ACTIVATES
OF A NUMBER OF LIVER GENES SUCH AS HNF3B.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 1 CUT HOMAIN.
SIMILARITY: BELONGS TO THE CUT HOMEOBOX FAMILY.
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19; Conser
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                                                                                                                       PS00027; HOMEOBOX_1; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                             and this statement is not removed
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235
943 AA;
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ulation; Homeobox; DNA-binding; Nuclear protein;
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Primates;
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                             CUT.
HOMEOBOX.
POLY-GLY.
POLY-PRO.
POLY-ALA.
POLY-HIS.
POLY-SER.
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Score 57;
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23;
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Pfan; PP00884; Sulfatase.
PF0884; Sulfatase.
PROSITE; PS00523; SULFATASE.1; 1
PROSITE; PS00149; SULFATASE.2; 1
Hydrolase; Complete proteome
INIT_MET
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P51691;
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Nature 406:959-964(2000).
-i- FUNCTION: SHOWS MAXIMAL ACTIVITY AT 57 DEGREES CELSIUS AND INCUBATION THAT OVERSTEPS 20 MINUTES ABOVE 50 DEGREES CELSI
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and characterization of the arylsulfatase synthesized by Pseudomonas aeruginosa PAO during growth in sulfate-free medium and cloning of the arylsulfatase gene (atsA)."; Eur. J. Biochem. 229:385-394(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL S
STRAIN-ATCC 15692 / PAO1;
MEDLINE-95262702; PubMed-7744061;
                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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Kertesz M.A.;
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Bacteria; Proteobacteria;
                                                                                                 EMBL; AE004456; AAC
HSSP; P15848; 1FSU.
                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
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Submitted (AUG-1999)
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                              EMBL; Z48540; CAA88421.2;
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                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: A phenol sulfate + H(2)0 SUBUNIT: MONOMER. SUBUNIT: MONOMER. SUBCELLULAR LOCATION: Cytoplasmic (Potential) SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                     INCUBATION THAT OVERSTEPS 20 MINUTES LEADS TO ENZYME INACTIVATION.
                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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Best Local
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CONFLICT
SEQUENCE
                                       Schiffer C.A., Clifton I.J., Davisson V.J., Santi D. "Crystal structure of human thymidylate synthase: a mechanism for guiding substrates into the active sit Blochemistry 34:16279-16287(1995).
                                                                                 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE-96110704; Pubmed-8845352;
                                                                                                                                Shimizu K., Ayusawa D., Takeishi K., "Purification and NH2-terminal amino thymidylate synthase in an overproduc
                                                                                                                                                     MEDLINE-85261174; Pubmed-3839505;
MEDLINE-85261174; Pubmed-3839505;
                                                                                                                                                                                                  "Human thymidylate synthase gene: iso cover a functionally active gene and region upstream from the translation J. Blochem. 106:575-583(1989).
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15-JUN-2002
         X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-21229106; PubMed-11329255;
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Takeishi K., Kaneo
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Takeishi K., Kaneda (
"Nucleotide sequence
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Eukaryota; Metazoa; Chordata; Craniata; Hominidae,
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                                                                                                                  Biochem.
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13; Conservative
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                                                                                                                 97:845-850(1985).
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Kaneda S., Ayusawa D
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toglu J., Takeishi K.,
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da S., Ayusawa D.
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Dunlap R.B.,
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Q13526;
                                                                                                                                                                                                                                                                                                                                                     _HUMAN
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
(Rotamase Pin1) (PPIase Pin1).
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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of human thymidylate synthase suggests chemotherapy with noncompetitive inhibitors.";
J. Biol. Chem. 276:14170-14177(2001).
Ľ
                       MEDLINE-96195064;
                                         SEQUENCE FROM N.A.
                                                                                Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                          Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0108; THYMDSNTHASE.
PRODOM; PD001180; Thymidylat_synt; 1.
PROSITE; PS00091; THYMIDYLATE_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1HW3; 09-MAY-01.
PDB; 1HW4; 09-MAY-01.
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PIR; A23047; YXHUT.
PDB; 1HVY; 31-JAN-01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-21216721; PubMed-11278511;
Phan J., Steadman D.J., Koli S., Ding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 40:1897-1902(2001).
                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Methyltransferase; Nucleotide biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
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K.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Deoxyribon SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3iol. Chem. 276:14170-14177(2001).
CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X02308; CAA26178.1; -. D00596; BAA00472.1; -.
                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC002567; AAH02567.1; -. BC013919; AAH13919.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
Hanes
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312 AA;
                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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S.D.,
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                    PubMed=8606777;
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35584 MW;
                                                                                                          Chordata;
Primates;
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Hunter
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Pred. No. 9.6;
7; Mismatches
                                                                                                          Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                            Hominidae;
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                                                                                                                                                                                                                      CEC
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                                     H_CHICK
HMPH_CHICK
Q05502;
Q1-JUN-1994
Q1-JUN-1994
Q1-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U49070; AAC50492.1; -. EMBL; BC002899; AAH02899.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00639; Rotamase; 1. PRINTS; PR00403; WWDOMAIN. SMART; SM00456; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           suggests substrate recognition is phosphorylation cell\ 89:875-886(1997).
                      Homeobox
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001202; Pfam; PF00397; WW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000297; Rotamase.
InterPro; IPR002349; WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 601052
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"Structural and functional analysis of the mitotic rotamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97344079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human peptidyl-prolyl
tosis ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Essential PPTase that regulates mitosis presumably by interacting with NIMA and attenuating its mitosis-promoting activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ween the Swiss Institute of Bioinf European Bioinformatics Institute
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CATALYTIC ACTIVITY: Peptidylproline
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een the Swiss Institute of Bioinformatics and the El
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  ox protein PRH.
gallus (Chicke
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15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS01096; PPIC_PPIASE_1;
PS50198; PPIC_PPIASE_2;
PS01159; WW_DOMAIN_1; 1.
PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                           GKNGQGEPARVRCSHLL----VKHSQSRRPSSWRQEKITRT
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                                         (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          525
    (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                 163 P
; 18243 MW;
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                                                                                                                                                                                                                                                                                                                         21.5%;
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                                       Created)
Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein;
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                                                                                                                                                                                                                                                                                                                           Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                   PPIC.
; 35391AF40B7D1E13 CRC64;
                                                                                                                                                                                                                                                                                                          Mismatches
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01-OCT-1994 (Rel. 3
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
0-succinylbenzoic a
                  SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-2134948; PubMed-11677609;
MCClelland M., Sanderson K.E., Spieth J.,
Courtney L., Porwollik S., Ali J., Dante M.
Leonard S., Nguyen C., Scott K., Holmes A.,
Ryan E., Sun H., Florea L., Miller W., Sto
                                                                                                                                                                                                                         Salmonella typhimurium.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÷
Waterston R.,
                                                                                                                                                                                   NCBI_TaxID=602;
                                                                                                                                                                                                        Salmonella
                                                                                                                                                                                                                                                                (O-succinylbenzoate-CoA MENE OR STM2305
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STANDARD;

PRT;

455

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30, Created)
41, Last sequence update)
41, Last annotation updat
acid--CoA ligase (EC 6.2.

ion update) (EC 6.2.1.26)

(OSB-CoA synthetase)

synthase).

gamma subdivision;

Enterobacteriaceae

eth J., Clifton S.W., Latreil
Dante M., Du F., Hou S., Layr
olmes A., Grewal N., Mulvaney

Latreille S., Layman

Layman

Stoneking

T.,

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SELECTION OF THE RESERVE OF COCCOCCOCCE THE SERVE OF COCCOCCE THE 
                                                                                                                                     Query Match
Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93087175; PubMed=1360645; Crompton M.R., Bartlett T.J., Macgregor A.D., Buratti E., Gianoctti V., Goodwin G.H.; "Identification of a novel vertebrate homeobox haematopoietic cells."; Nucleic Acids Res. 20:5661-5667(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93087175;
Crompton M 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X64711; CAA45966.1; -. HSSP; P22808; 1NK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T02091; -.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                    Homeobox; DNA-binding; Developmental protein; Nuclear protein
DOMAIN 1 140 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN HEMATOPOIETIC DIFFERENTIATION.
SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: IN ALL HEMATOPOIETIC TISSUES EXCEPT PERIPHERAL BLOOD ERYTHROCYTES AND IN THE LIVER AND LUNG.
125 DPLGKPLLWSPFIQRPLHKRKGGQVRFS
                                                     μ.
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00024; HOMEOBOX.
                                                  EPLGPRGQDSPLLQRPQHLMDQGQMRHS
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277 i
                                                                                                              Conservative
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30213 MW;
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                                                                                                                                        21.5%;
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••
                                                                                                                                        Score 56;
Pred. No.
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BE744C143FB9F9FC CRC64;
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9.7;
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RESULT
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Best Local S
Matches 17
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Q9UJV9; Q96BK6; (Rel
16-OCT-2001 (Rel
15-JUN-2002 (Rel
15-JUN-2002 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple copies.
J. Bacteriol. 17
-i- FUNCTION: O-
      Isogai T., Ota T., Hayashi K.,
Nishikawa T., Nagai K., Sugano
Wagatsuma M., Hosoiri T., Kaku
Takahashi M., Chiba Y., Ishida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
[2]
                                                                   TISSUE-Placenta;
                                                                                                                                    X
                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=20076860;
                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             StyGene; SG10221; menE. InterPro; IPR000873; A
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between the Swiss Ins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94266712; PubMed=8206837;
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                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                               "Tevelopmental and cell biological
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- FUNCTION: O-SUCCINYLBENZOIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
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PATHWAY: Menaquinone biosynthesis.
SIMILARITY: BELONGS TO THE ATP-DEPEN
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CATALYTIC ACTIVITY: ATP + O-succinylbenzoate
                                                                                                                                    protein
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U02281; AA
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                                                                                                                     Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLGPRGQDSPLLQRPQ-HLMDQGQMRHSFSAGPELLRQDKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biosynthesis; Ligase;
455 AA; 50244 MW; BC
                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                 abstrakt.";
9:1373-1381(1999)
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AAA21323.1; -.
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Q9NW04; Q96K05;
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                                                                                                                                                                                  PubMed=10607561;
                                                                                                                                                                                                                                               ; Chordata;
; Primates;
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Pred. No. 20;
4; Mismatches
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                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae
      Sugiyama T., Otsuki T.,
S., Shiratori A., Sudo I
Y., Kodaira H., Kondo H
S., Murakawa K., Ono Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-DEPENDENT
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when
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Homo.
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    , Sugawara
Takiguchi
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60S_ribosoma
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Yamamoto J., Wakamatsu
Ninomiya K., Iwayanagi
"NEDO human cDNA sequen
          Saccharomyces
                    NO425).
                             (RPL18A
                                                                                                                                                                                                                                                                                                CONFLICT
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ATP-binding;
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Pfam; PF00271; helicase_C;
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                       Local
                           ween the Swiss Institute of Bioinf. European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: PROBABLE ATP-DEPENDENT RNA HELICASE. IS REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POST-TRANSCRIPTIONAL GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright.
een the Swiss Institute of Biol
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AK001255;
AK027768;
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Q58083; 1
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                                                                                                                                                                                                                                                                                                                                   PS00039; DEAR TO
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(MAY-2001) to t
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es cerevisiae
Fungi; Ascomyc
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225 232
344 347
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Iwayanagi T.;
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31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                   Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                          DEAD_box
                                      Last
L18 (
                                                          Last
                                                                    Created)
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         (Baker's
                                        (RP28)
                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                              Helicase; Nuclear pro
                                               sequence update)
annotation updat
                                                                                                                                                                              10;
                                                                                                                                                                                                                           PAGGSRSEAEDEDDEDYVPYVPLRORR ->
MRTTRITCPMCRYAAP (IN REF. 1).
K -> E (IN REF. 2; BAA51585).
Q -> E (IN REF. 2; BAB53355).
K -> E (IN REF. 2; BAB53355).
A -> T (IN REF. 2; BAB91585).
M -> T (IN REF. 2; BAB91585).
L -> Q (IN REF. 2; BAB53355).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura
                                                                                                                                                                          Score 55.5; un
Pred. No. 28;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       project.";
EMBL/GenBank/DDBJ
                             AND
                                                                                                                                                                                                                                                                                                                      ΑTΡ
                                                                                                                                                                                                                                                                                                           DEAD
  Saccharomycotina;
                                                                                        PRT;
                                                                                                                                                                                                                    E0A328724E0DF99A
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                             (RPL18B OR RP28B
                                                                                                                                                                                                                                                                                                            BOX
          yeast)
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                                                 update)
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                                                                                                                                                                                                 DB
                                                                                                                                                                                                                    2; BAA91585).
2; BAA91585).
2; BAB55355).
99A CRC64;
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  Saccharomycetes
                                                                                                                                                                                               Length
                              OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration
Coutstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
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RESULT 14
ATS9_HUMAN
ID ATS9_AC Q9P2N
DT 16-OC
DT 16-OC
DT 15-JI
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
ATS9_HUMAN STANDARL
Q9P2N4; Q9NR29;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
15-JUN-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lafuente M.J., Gamo F.J., Gancedo C.;
"DNA sequence analysis of a 10 624 bp fragment of the left arm of chromosome XV from Saccharomyces cerevisiae reveals a RNA binding protein, a mitochondrial protein, two ribosomal proteins and two ropen reading frames.";
Yeast 12:1041-1045(1996).

1- MISCELLANEOUS: THERE ARE TWO GENES FOR L18 IN YEAST.
1- SIMILARITY: BELONGS TO THE L18E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
PIR;
SGD;
SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
"Sequence analysis of a 30 kb DNA segment from yeast chromosome carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, a novel putative serine/threonine protein kinase gene.";
Yeast 11:1303-1310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96132033; Pub
                                                                                                                                        HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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Nucleic Acids Res. 12:7345-7358(1984);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (RPL18A AND RPL18B). MEDLINE-85037916; PubMed-6387623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BL; X01099; CAA25573.1; -.
BL; X01635; CAA26481.1; -.
BL; X01100; CAA25574.1; -.
BL; Z01100; CAA25574.1; -.
BL; Z71577; CAA96219.1; -.
BL; Z71577; CAA96219.1; -.
BL; Z74862; CAA64550.1; -.
BL; Z74866; CAA64550.1; -.
BL; Z74866; CAA699139.1; -.
BL; Z74867; RFL18B.
BL; Z74867; RFL18B.
C; S0005248; RFL0S0MAL_L18E; 1.
CSITE; PS01106; RIBOSOMAL_L18E; 1.
OSSITE; PS01106; RIBOSOMAL_L18E; 1.
DOSSOMAL DISCALL; MILTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                       PRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTG 48
                                                                                                                                                                                                                                              PKGQNTLILRGPRN--SREAVRH-FGMGP---HKGKAPRILSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
186 AA;
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8553702;
banus J.H.M., Planta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene
20563 MW;
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                                                       Created)
  Last sequence up
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Pred. No. 8;
10; Mismatches
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linked
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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        PROSITE; PS50215;
PROSITE; PS00427;
PROSITE; PS50092;
PROSITE; PS00142;
  Hydrolase;
Repeat; Ex
                                                                                                                                                                                                                                         InterPro;
Pfam; PFO
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                                                                                                                                                           Pfam; PF00090; tsp_1; 11. fram; PF011421; Reprolysin; 1. pfam; PF011421; Reprolysin; 1. pfam; Pf011562; Pep_M12B_propep; smarr; SM00209; TSP1; 12.
                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF261918; AAF89106.1;
EMBL; AB037733; BAA92550.1;
HSSP; P15167; 1ATL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara ("Prediction of the coding sequences of unidentified human The complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from brain with the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the complete sequences of 150 new cDNA clones from the compl
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics
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                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) A ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING. SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ALL FETAL TISSUES. EXPRESSED SLIGHTLY IN ADULT OVARY, PANCREAS, HEART, KIDNEY, PLACENTA. ALSO DETECTED IN SPINAL CORD AND BRAIN. NOT DETECT OCLON, SMALL INTESTINE, TESTIS, LIVER, SKELETAL MUSCLE, SPLICLON, SMALL STANDARD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1:
SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DON
SIMILARITY: CONTAINS 11 TSP TYPE-1 DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Res. 7:65-73(2000).
COFACTOR: BINDS 1 ZINC ION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
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PTM: THE PRECURSOR
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FOR A TIGHT
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             TSP1; 9.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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ATZS2 OR AT4G27150 OR T24A18.100.
Conceicao A.D.S., Krebbers
         STRAIN-CV.
                SEQUENCE FROM N.A.
                                Plant
                                                Vandekerckhove J.; "Determination of the
                                                                 van Damme J., Segura
                                                                         Krebbers E., Herdies
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                                                                                                          NCBI_TaxID=3702;
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RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Trancs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Scheking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Berthof J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Nelson J., Spieth M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
Thalian M., Strong C., Stocker S., Geisel C., Layman D.,
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A Van der Schueren J. Grymonprez B. Chuang Y.-J. Vandenbussche F.
A Braeken M. Weltjens I. Voet M. Bastiaens I. Aert R. Defoor E.,
A Weitzenegger T. Bothe G. Ramsperger U. Hilbert H. Braun M.
A Holzer E. Brandt A. Peters S. van Staveren M. Dirkse W.,
A Mooijman P. Klein Lankhorst R., Rose M. Hauf J. Koetter P.,
Berneiser S. Hempel S. Feldpausch M. Lamberth S. Van den Daele H.,
A Berneiser S. Hugsshaert C. Gielen J. Villarroel R., De Clercq R.,
A Clark L. Doggett J. Hall S. Kay M., Lennard N., McLay K., Mayes R.,
A Clark L. Doggett J. Hall S., Kay M., Lennard N., McLay K., Mayes R.,
A Clark L. Doggett J. Hall S., Kay M., Lennard V., Rechmann S.,
A Clark L. Doggett J. Hall S., Kay M., Benes V., Rechmann S.,
A Clark L. Doggett J. Hall S., Kay M., Lennard N., McLay K.,
A Borkova D. Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
A Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
A Borkova D., Herzl A., Vitale D., Liguori R., Piravandi E.,
ARA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
A Nassenet C., Quigley F., Clabauld G., Muendlein A., Felber R.,
A Chashl C. Hiller B. Cohmitt W. Incharny A. Anhonirg S.
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Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.
Weichselgartner M., de Simone V., Obermaler B., Mache R.,
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                                                                                                                                                                                                                                                                                                  mal M., Grellet F., Laudie M., Meyer Y., Cooke R., Dumitted (OCT-1992) to the EMBL/GenBank/DDBJ databases FUNCTION: THIS IS A 2S SEED STORAGE PROTEIN.
SUBDUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND LINKED BY DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS
                                                                                                                                                                                                        ween the Swiss Institute of Bioinformatics Institute.
; M22034; AAA32744.1;
; Z24745; CAA80871.1;
; AL035680; CAB38845.1
; AL161566; CAB79570.1
                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                               an email to license@isb-sib.ch).
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CAB38845.1; CAB79570.1;

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Search completed: June 17, 2003, 11:56:49 Job time: 3.94143 secs
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EMBL; Z17594; CAA79008.1; -.
PIR; JA0162; NWMU2.
PIR; S34677; S34677.
InterPro; IPR003612; AAI.
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InterPro; IPR001768; Try/amyl_inhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
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   671580 seqs, 206047115 residues
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Q9ybml aeropyrum p
Q9r1x2 mus musculu
Q9crv1 mus musculu
Q9acr4 streptomyce
Q9nrr6 homo sapien
Q85275 potato viru
Q9c264 neurospora
Q96wj2 kluyveromyc
Q24593 drosophila
Q9w425 drosophila
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Q9ulh6 homo sapien
Q9hul9 pseudomonas
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## ALIGNMENTS

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RESULT 2
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O9ULH6 PRELIMINARY; PRT;
O9ULH6; O96P46;
O1-MAY-2000 (TIEMBLrel. 13, Created
O1-MAY-2000 (TIEMBLrel. 13, Last se
O1-JUN-2002 (TIEMBLrel. 21, Last ar
KIAA1244 protein (BIG3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (SEP-2001) to the
EMBL; BC014227; AAH14227.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 66.4 kDa protein (Fragment).
                                                                                                                                                                       592 AA; 66400 MW;
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"KIAA1244 as a novel distantly results and yet of ARF GEFs.";

Subfamily of ARF GEFs.";

Submitted (AUG-2001) to the EMBL, EMBL, AB033070; BAA66558.1;

EMBL; AB033070; BAA66558.1;

EMBL; AF413080; AAL04174.1;

InterPro; IPR000904; Sec7.
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Brith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:999-964(2000).
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Prediction of the coding sequences of
The complete sequences of 100 new cDNA
for large proteins in vitro.";
DNA Res. 6:337-345(1999).
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InterPro; IPR002078;
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16, Last
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Catarrhini;
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Pred. No. 2.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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R INTERACTION ATP
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Best I
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                                                            Query Matc
Best Local
                                           Matches
                                                                                                                      Newfeld S.J.;
Submitted (May-1992) to
EMBL; M92914; AAC37201.:
FlyBase; FBgn0013119; by
SEQUENCE 1655 AA; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q24754;
Q24754;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PR01590; HTHPIS.
ProDom; PD000039; Response_re;
SMART; SM00382; AAA; 1.
SMART; SM00448; REC; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropo
Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
PROSITE; PS00685; SIGMA54_INTERACT_4; 1.
ATP-binding; DNA-binding; Phosphorylation; Transcription regulation; Complete proteome SEQUENCE 462 AA; 50864 MM; 981D88847B2B
                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=94111143; PubMed-8283480;
Newfeld S.J., Schmid A.T., Yedvob
"Homopolymer length variation in
J. Mol. Evol. 37:483-495(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mastermind.";
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01-JUN-2001
                                                                                                                                                                                                                                                                                                     Newfeld S.J., Tachida H., Yedvobnick B.; "Drive-selection_equilibrium: homopolymer
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=94365848; PubMed=8083889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newfeld S.J., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91251140;
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                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                     mastermind.";
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16; Conserv
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                                                                                                                                                                                                                                                                  Evol.
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                                                                                                                                                                                                                        FROM N.A.
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|| ||:| ||| | : | ||| : |
PLRERGEDIPLLFR--HFAEAGAMRHGLT
  PLGPRGQDSPLLQRPQHLMDQGQMRHSFSAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virilis (Fruit fly).
Metazoa, Arthropoda; Tracheata; He
Meoptera; Endopterygota; Diptera;
Neoptera; Childae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
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                                                                                                                                                                                                                                                                                                                                                                                                     , Schmid A.T., Yedvobnick length variation in the l. 37:483-495(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smoller
                                                                                                                                                                                                                                                                  38:637-641(1994).
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27.6%;
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175048 MW;
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17,
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Last sequence up
Last annotation
                                       Score 62.5; I
Pred. No. 16;
9; Mismatches
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unusually
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3.3;
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a; Brachycera; Musc
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Q9X6T3
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Matches
Query
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                                                                                                                                                                                                              MEDLINE-20036896; PubMed-10567266;
Mhite O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.J. Makarova K.S., Aravind L., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9RT11; PRELIMINARY; O9RT11; 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001)
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01-NOV-1999
01-JUN-2001
                                    Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyun C.G., Suh J.W.;
"Isolation of the genes for glycosyltransferase and N-methyltransferase from Streptomyces spectabilis ATCC277, spectinomycin producer.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF145038; AAD28487.1;
TEMBL; AF145038; AAD28487.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces spectabilis.

Streptomyces spectabilis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                       InterPro; IPR000209; Peptidase_S8
PROSITE; PS00136; SUBTILASE_ASP; (
                                                                                                          EMBL; AE002034; AAF11509.1;
TIGR; DR1958; -.
                                                                                                                                                 radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                      "Genome sequence of the radioresistant
radiodurans R1.";
                                                                                                                                                                                                       Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcaceae;
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Thermus/Deinococcus Deinococcaceae; Deinococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales;
NCBI_TaxID=68270;
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Pfam; PF00535; Glycos_transf_2; 1.
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9 (TrEMBLrel. 12,
1 (TrEMBLrel. 17,
                                  Complete proteome. 333 AA; 34881 MW;
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Pred. No.
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                                    47042A084B54D638
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60;
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                                    CRC64;
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Length 333;
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                                                                                                                                                                                                                                                                                                                 J.D.,
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RESULT 8
Q9R1X2
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Q9YBM1
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Best Local S
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99310339; PubMed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., K. Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                         Hex.
                                                                   STRAIN-129; TISSUE-LIVER
Myint Z., Inazu T., Tana
Kuriyama M., Noguchi T.;
                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crenarchaeon, Aeropyrum pernix K1.";
DNA Res. 6:83-101(1999).
EMBL; AP000062; BAA80577.1; -.
            Submitted (AUG-1998) to the -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9YBM1;
                                                                                                            SEQUENCE
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                        HHEX OR HEX (PRH)
                                                                                                                                                                                                                                                              Q9R1X2;
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SEQUENCE 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum pernix.
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                                                                                                                                   NCBI_TaxID=10090;
                                                    "Genomic
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                                                                              E FROM N.A.
129; TISSUE-LIVER;
Tanak
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rel. 20, L
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31.9%;
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13,
20,
                                                    promoter analysis
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Pred. No. 7;
8; Mismatches
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Last annotation update)
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7; Mismatches
                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
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CF1D95C2B17E92E8
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annotation update)
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              SIMILARITY).
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                                                                                V.W.,
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                                                                                                                                                   Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
             PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                   MGD; MGI:96086; Hhex. InterPro; IPR001356; Homeobox.
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InterPro; IPR001356; Homeobox.
 DNA-binding;
                                                                      Pfam; PF00046; homeobox; 1 PRINTS; PR00024; HOMEOBOX.
                                                                                                                                              - I - SUBCELLULAR LOCATION: NUCLEAR EMBL; AK014111; BAB29163.1; -.
                                                                                                                                                                         "Functional annotation o
Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CRV1;
                                             SMART;
                                                       ProDom; PD000010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                          Hayashizaki Y
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                                                                                                                                P22808; 1NK3
                                         ; PD000010; Homeobox; 1.
SM00389; HOX; 1.
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16; Conserv
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(TrEMBLrel. 17,
(TrEMBLrel. 20,
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BAA76714.1;
BAA76714.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed
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Rodentia;
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Nuclear protein
                                                                                                                                                                                         of a full-length mouse cDNA
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Last annotation update
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Sciurognathi;
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4C0AD438CCAAA6F4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata;
thi; Muridae;
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                                                                                                                                                                                          collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Mus
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Fukuda S.,
amanaka I.,
Saito R.,
                                                                                                                                                                                                                                  Wilming
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Best Local
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Q9ACT4;
Q1-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SCP1.217.1C.
SCP1.217.1C OR SCP1.217AC.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL590464; CAC36740.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 381 AA; 40037 MW; 45B3D68D962B7525 CRC64;
                   "The Isolation and Characterization of a c
                                                                 TISSUE=BRAIN;
MEDLINE=20347929;
                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                     Phosphatidylinositol polyphosphate
                                                                                                                                                                                                                                                                                                                         Q9NRR6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                         Q9NRR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid
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                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                       Mammalia;
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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDSPLLQRPQHL--MDQGQMRHSF----SAGPELLRQ--DKRPRSGSTG
                                                                                                                                                                                  Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Polyphosphate
                                                                 PubMed=10764818;
                                                                                                                                                                                    Primates;
                                                                                                                                                                                                            Chordata;
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36.7%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB
Pred. No. 9.2;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
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Pred. No.
                                                                                                                                                                                  Catarrhini;
                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9405DC67E1842FF0 CRC64;
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5-Phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycetaceae;
                                                                                                                                                                                                                                                        5-phosphatase type
                                                                                                                                                                                                                                                                                                                                                                         644
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a cDNA Encoding phatase.";
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5.5;
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9.2;
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                                                                                                                                                                                    Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 381;
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                     Phospholipid-
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Howarth S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379
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Best Local S
Matches 19
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Matches 18
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Q85275;
                                                                                                         Neurospora crassa.
Eukaryota; Fungi; Ascomycota;
Sordariales; Sordariaceae; Ne
                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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InterPro;
InterPro;
Schulte U., Aign V.,
Nyakatura G., Mewes I
Submitted (FEB-2001)
                                                                                                                                                                                                                                                                 Q9C2E4;
                                                                                                                                                                                                                                                                                     Q9C2E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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InterPro: IPR002540; Poty_Pl; 1.
Pfam; PF01577; Poty_Pl; 1.
NON_TER 276 276
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                       Related to vacuolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X82848; CAA58051.1;
                                                      SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S30.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Potato plants transformed with a resistant to PVY-O.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potato virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-12216;
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                                                                                                                                                                                                                                                                                                                                                                                117
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AF187891; AAF81404.1; -.
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Maki-Valkama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELL - - RQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00294; PRENYLATION; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                            EPQAPRGIIHTTPRVRKVKTRPIIKLTEGQMDH-----LIKQVKQIMSGKRGS
                                                                                                                                                                                                                                                                                                                                                                                                            EPLGPRG--QDSPLLQ----RPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIAPRPPARPRLERALSLDDKGWRRRRFRGSQEDLEARNGTSPSRGSVQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR005135; Exo_endo_phc
IPR000300; IPPc.
IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOV-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276. AA;
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                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
, Hoheisel J., Brandt P., I
H.W., Mannhaupt G.;
) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                     protein
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19,
20,
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01,
19,
                                                                                                             la; Pezizomycotina;
Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 59; DB;
; Pred. No. 17;
3; Mismatches
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Last sequence update)
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sorting-associated prot
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Pred. No. 7.
                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00A74C8425D5F2BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potato virus Y
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17;
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                                       В.,
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                                       Holland
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Best Local S
Matches 13
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Best Local
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Q24593;
Q14593;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 20, L
Q1-NAR-2002 (TrEMBLrel. 20, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Schmuck E.M., Chen X.J.;
Schmuck E.M., Chen X.J.;
"The yeast PRM1 gene is involved in resistance to paromomycin.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF285275; AAK69551.1; -
EMBL; AF285275; AAK69551.1; -
SEQUENCE 778 AA; 88129 MW; 6262CFEA6B178B44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96WJ2;
                                                                                                                                                                                                                                                                                                                  Pterygota; metazoa; Arthropoda; Tracheata; H. Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila. NCBL TaxID-7227.
                                                                                                                                                                                                                                                                                                                                                                                                                             WD-40 repeat protein ANON-X.
CG3585 OR ANON-X OR DMX.
Drosophila melanogaster (Fruit fly)
                                     repeat protein.";
Gene 216:267-276(1998)
-!- SIMILARITY: CONTAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001683; Pfam; PF00787; PX; 1 SMART; SM00312; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   German Neurospora genome pr
Submitted (NOV-2001) to the
EMBL; AL513463; CAC28769.2;
         EMBL;
                                                                                                                           MEDLINE~98398448; PubMed~9729422;
Kraemer C., Weil B., Christmann M.
"The new gene DmX from Drosophila
                                                                                                                                                                                                                      STRAIN-506RY;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales;
NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paromomycin-resistance
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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         x97196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conserv
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13; Conserv
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      Y: CONTAINS CAA65830.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64100 MW;
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Pred. No. 24;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred. No. 17;
7; Mismatches
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                                     REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                             Schmidt
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                                     (TRP-ASP DOMAINS)
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a; Brachycera;
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DR FlyBase; FBgn0023458; CG3585.

DR InterPro; IPR002106; AAKRNA_ligaseII.

DR InterPro; IPR000217; Tubulin.

DR PGSITE; PS00320; WD40; 7.

DR PROSITE; PS00320; WD40; 7.

DR PROSITE; PS00027; TUBULIN; 1.

DR PROSITE; PS00027; TUBULIN; 1.

DR PROSITE; PS00027; WD_REPEATS_1; UNKNOWN_1.

DR PROSITE; PS00028; WD_REPEATS_2; 1.

DR PROSITE; PS000294; WD_REPEATS_2; 1.

DR PROSITE; PS000294; WD_REPEATS_REGION; 1.

KW Repeat; WD repeat.

SQ SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

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SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

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SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

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SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

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SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

Query Match

SEQUENCE 3429 AA; 377671 MW; 4857FC939B8A13B9 CRC64;

SEQUENCE 3
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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215
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Match
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Gapop 10.0 , Gapext 0.5
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518
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1807
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388
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 AAM50812
AAM85472
AAM509728
ABG09731
ABG09731
AAU36030
AAW98375
AAW98375
AAW98375
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PS118 protein enco
PS118 prostate mar
Novel human diagno
Novel human diagno
Helicobacter pylor
Mouse oocyte prote
H. pylori GHPO 113
Helicobacter pylor
Arabidopsis thalia
                                                                                                                                                                                                 Description
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AAM50812
ID AAM5
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AC AAM5
AC AAM5
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ABB91690 AAG50356 AAG50355 AAG50355 AAG50355 AAG92796 AAG18381 AAG11287 AAG118381 AAG11287 AAG881158 AAG88	50369 44031 50368 50367
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## ALIGNMENTS

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PA	PA	PA	PA	PA	PA	PA	PA	PA	×	PR	×	PF.	×	PD	×	NG	XX	S	×	ΚW	XX	X
_	(KLAS/) KLASS M R.	(HODG/) HODGES S.C.	(GRAN/) GRANAL	(GORD/) GORDON J.	(FRIE/) FRIEDM	(COPL/) COPLPI	(COHE/) COHEN M	(BILL/) BILLIN		23-APR-1997;		23-APR-1998;		27-DEC-2001.		US2001055758-A1		Homo sapiens.		prostatitis; h	benign prostat	PS118; prostat
KRATOCHVIL J D.	M R.	s.c.	GRANADOS E N.	I J.	FRIEDMAN P N.	COPLPITTS T L.	Χ.	BILLING-MEDEL P A.		97US-0842385.		98US-0065383.				1.				prostatitis; human; diagnosis; therapy; vaccine; immunogen.	benign prostatic hyperplasia; prostatic intraepithelial neoplasia;	PS118; prostate; marker; prostate cancer; tumour; metastasis
		,,													1					lmmunogen.	nelial neoplas	metastasis;

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RESULT 2
AAW85472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
Billing-Medel PA, Cohen M, Colpitts TL,
Gordon J, Granados EN, Hodges SC, Klass
Robert-Srapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting presence of target PSI18 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granados EN,
Russell JC,
                                                                                                                                                                                      WO9848054-A1
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                             EST clone; PS118; prostate tumour tissue; prostatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-187683/24
                                                                                           23-APR-1997;
                                                                                                                         23-APR-1998;
                                                                                                                                                        29-OCT-1998
                                                                                                                                                                                                                                                                         PS118 protein encoded by consensus sequence
                                                                                                                                                                                                                                                                                                         25-FEB-1999
                                                                                                                                                                                                                                                                                                                                     AAW85472;
                                                                                                                                                                                                                                                                                                                                                                 AAW85472 standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ROBE/) ROBERTS-RAPP L.
                                                             (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         μ
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N, Hodges SC,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ξ</u>
                                                             LAB
                                                                                           97US-0842385
                                                                                                                        98WO-US08239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 215; DB 23;
Pred. No. 2.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
               Friedman
MR, Krat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                  Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Roberts-Rapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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RESULT 3
AAM50809
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
                     Billing-Medel PA, Co
Granados EN, Hodges
Russell JC, Stroupe
                                                                                                                                                                                                                                                                                                                                 benign prostatic hyperplasia; prostatitis; human; diagnosis;
                                                                                                                                                                                                                                                                                   US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                PS118 prostate marker partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50809
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM50809 standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 93-94; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Pl18 nucleic acid and proteins - used for diagnosis and treatment of prostatic disease, especially cancer, and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                    23-APR-1998;
                                                                                                                                                                                                                                                             27-DEC-2001.
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           PS118;
                                                                         (ROBE/)
                                                                                                                                                              (COPL/)
                                                                                                                                                                          (COHE/)
                                                                                                                                                                                       (BILL/)
                                                                                                 KLAS/)
                                                                                                              HODG/)
                                                                                                                           GRAN/)
                                                                                                                                                   FRIE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998-610000/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK
                                                                                                                                                                                                                                                                                                                                                         prostate;
                                                                                               GRANADOS E N. HODGES S C. KLASS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK
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                                                                                                                                     FRIEDMAN P N. GORDON J.
                                                                                                                                                                                     BILLING-MEDEL P A.
                                                                       ROBERTS-RAPP L.
                                                                                                                                                              COPLPITTS T L.
                                                                                                                                                                         COHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA;
                                                                                                                                                                                                             97US-0842385
                                                                                                                                                                                                                                      98US-0065383
                                                                                                                                                                                                                                                                                                                                                         marker; prostate cancer; tumour; metastasis;
                      Cohen
ges SC,
upe SD;
                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                 diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                   M, Coplpitts TL, Friedma
Klass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 215; DB 19;
Pred. No. 4.3e-20;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                              intraepithelial neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clones AAV82803-10.
                                                Friedman PN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                   Roberts-Rapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518;
                                                Gordon J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived
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WPI; 2002-187683/24

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                             food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 42-43;
                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                  30-MAR-2001;
                                                                                                                                                                                                                                                  11-OCT-2001
                                                                                                                                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #9719
                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG09728 standard; Protein; 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABA91651.
                                                              2001-639362/73.
DB; AAS73915.
                                                                                                                                                                                                                                                                                                                                           supplement;
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                                                                                                         RT,
                                                                                                                                        HYSEQ
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                                                                                                                                                                     2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                   2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Å
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                                                                                                                                                                                                                                                                                                                                        e mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
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                                                                                                         Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 215; DB 23;
Pred. No. 4.3e-20;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371
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RESULT 5
ABG09731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc polynucleotides are also used in diagnostics as expressed sequence tags cfor identifying expressed genes. (I) is useful in gene therapy techniques ct to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or creating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cmaning of sittes expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. ABGO0010-ABG30377 represent novel human conditions and activities of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide (II) sequences. (I) is useful as hybridisation polymerase chain reaction (PCR) primers, oligomers, and for and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                       N-PSDB;
                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                              31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                           30-MAR-2001;
                                                                                                                                                                                                                                                                          11-OCT-2001.
                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #9722
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG09731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG09731 standard; Protein; 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1621
                                                                                     2001-639362/73.
DB; AAS73918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; SEQ ID No 40087; 103pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                           2001WO-US08631.
                                                                                                                                                                                              2000US-0540217.
2000US-0649167.
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Pred. No. 1.7e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful as hybridisation probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Claim 20;

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Best Local :
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                                                                                                                                                                                                                     21 MAR 2000; 2000US 191078P.
23 MAY 2000; 2000US 206848P.
26 MAY 2000; 2000US 207727P.
23 OCT 2000; 2000US 242578P.
27 NOV 2000; 2000US 25365P.
22 DEC 2000; 2000US 25365P.
16 FEB 2001; 2001US 25931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
WPI; 2001-611495/70.
N-PSDB; AAS53889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                  Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001WO-US09180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori cellular proliferation protein #343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                    (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1735
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                                                                            Ohlsen
Xu HH;
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                                                                                                              Zyskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
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Pred. No. 1.9e-19;
Mismatches 0;
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                                                                                                                 Trawick
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                                                                                                              JD,
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New polynucleotides for the identification and development

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RESULT 7
AAE06034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to correct products of cellular proliferation, their use in identifying the company, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The color in the interior is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation for the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
The present sequence is mouse occyte protein 5 (MOP5). The present invention relates to egg specific surface proteins
                                                                                       New egg-specific surface proteins, useful as immunogens in a vaccine preparation for modulating fertility, particularly useful for producing antibodies for temporary, reversible contraception methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotics, comprise sequences of antisense nucleic acids
                                                     Claim 1; Page 32-35; 41pp; English.
                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                   Herr JC,
                                                                                                                                                                                                                                                      (UYVI-) UNIV VIRGINIA PATENT FOUND
                                                                                                                                                                                                                                                                                       20-JAN-2000; 2000US-0177123.
                                                                                                                                                                                                                                                                                                                           19-JAN-2001; 2001WO-US01718.
                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                               WO200153339-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse oocyte protein 5; MOP5; egg specific surface protein; vaccine; fertility; contraceptive; active immunisation; ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE06034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                             2001-465367/50
DB; AAD11617, AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLKLWWSNLQNSLFTLLPDKLANALRISDLPESYQ 25:
                                                                                                                                                                                                                   Coonrod SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq ID No 11623; 511pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein 5 (MOP5).
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                                                                                                                                                                 AAD11618.
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sin; immunogen;
sterilisation.
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Best Local S
Matches 10
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                         This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also used for the production of antibodies. The products can also be used for
                                                                                                                                                                                             New isolated Helicobacter polynucleotides - for the diagnosis, prevention and treatment infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis peptic ulcer disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (antigens) and nucleic acids encoding them. The proteins of the invention are involved in egg-sperm binding and fusion. They are useful as immunogens in vaccine preparation for modulating fertility. In particular, the proteins are useful for producing antibodies which are useful for temporary, reversible contraception methods. The contraceptive vaccine is especially useful for controlling fertility in human beings or agriculturally important livestock, cattle or pig. The invention also relates to the use of
                                                                                                                                                                     Claim 8; Page 571-573; 2054pp; English.
                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW98375 standard;
                                       Sequence
                                                                                                                                                                                                                                                    N-PSDB; AAX14094
                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9843478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW98375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sterilisation of female animals.
                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies against such antigens for active immunisation or
                                                                  detection
                                                                                                                                                                                                                                                                1998-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 EDPNRQSKWLQDEMAFCYTQAPHKTVSLIL 347
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                                        388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                 diagnosis
                                                                                                                                                                                                                                                                                        Kleanthous
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97US-0833457.
97US-0881227.
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No. 32;
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                                                                                                                                                                                                                                                                                      Oomen RP,
            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                           of Helicobacter
             19;
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                                    The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC promologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence represents an CC assential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this pattent did not form part CC format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-
16-FEB-
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antibiotic;
Sequence
                                                                                                                                                                                                                                                                                                                     Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori cellular proliferation protein #178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM
                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                     Seq ID No 11458; 511pp; English.
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; antibacterial;
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2000US-206848P.
2000US-20772P.
2000US-242578P.
2000US-257931P.
2000US-257931P.
2000US-269308P.
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Xu HH;
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Query Match Best Local Similarity

26.3%; 34.3%;

Score Pred.

56.5; No. 32;

В

Length 388

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99US-0138094 99US-0138540. 99US-0138847. 99US-0139119. 99US-0139452.	99US-0137222. 99US-0137528. 99US-0137502. 99US-0137724.	990S-0136021. 990S-0136392. 990S-0136782.	99US-0135353. 99US-0135629.	99US-0134941. 99US-0135124.	99US-0134768.	99US-0134221.	99US-0134218.	99US-0134256.	99US-0132487.	99US-0132485.	99US-0132484.	99US-0132048.	99US-0131449.	99US-0130510.	99US-01304//.	99US-0129845.	99US-0128234. 99US-0128714.	99US-0127462.	99US-0126264.	99US-0125788.	9905-0123180.	99US-0121825.	2000EP-0301439.			thaliana.	sequence.	on; gen	OLETU	1	(first entry)		standard; Protein; 2			RLKLWWSNLQNSLFTLLPDRLANALRISDLPESYQ	- 14	Conservative 5;
																										•		signal transduction pa etic mapping; gene exp	Tradment SEA ID E	CEO Th			219 AA.				TISKLMTEYK 4	Mismatches
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																									٠			<pre>ic pathway; l; promoter;</pre>										5; Gaps 1;
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09-AUG-1999; 09-AUG-1999; 10-AUG-1999; 11-AUG-1999; 12-AUG-1999;	5-AUG-1999 5-AUG-1999 6-AUG-1999	-1999 -1999 -1999	.999	-1999 -1999	-1999	1999	-1999	1999 2-1999	999	-1999	1-1999	-1999	1-1999	1999	999	1999	1-1999 1-1999	1999	999	L-1999 L-1999	L-1999	999	1999	L-199	199 -199	199 199	7-199 1-199	1-199 1-199	1-199	1-199	9	V-199	-JUN-199	-JUN-199	-JUN-199	-JUN-199	-JUN-199	N-199
99US-0147493 99US-0147935 99US-0148171 99US-0148319 99US-0148319	99US-014719 99US-014726 99US-014730 99US-014741	990S-014703 990S-014720 990S-014730	99US-014638 99US-014638	99US-014595 99US-014638	990S-014591	99US-014591	99US-014522 99US-014522	99US-014514 99US-014521	99US-014519	9905-014508	99US-014508	99US-014508	99US-014481 99US-014481	99US-014463	99US-014435 99US-014435	99US-014433	99US-014433	99US-014433	99US-014408	99US-014408	9905-014362	99US-014297 99US-014354	9905-014292	9US-014239	9US-014215	9US-014128 9US-014184	9US-014082 9US-014099	90S-014035 90S-014069	9US-013989	9US-013981	9US-013976	9US-013946	9US-013946	9US-013945	9US-013945 9US-013945	9US-013945	9US-013945	908-013945

pathway;
promoter;

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35-OUT 1999
36-OUT 1999
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31-AUG                                   105
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                                                                                        th 26.0%;
Similarity 33.3%;
10; Conservative
                                                PSRKKEWWENAGNKIYTMAADKTISKLMTE
                                PSLQKQWYSVLGNHDYRGNVEAQLSKVLTQ 134
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9905-0150868
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99US-0149929.
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99US-0149930
                                                                                        8; Mismatches
                                                            38
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                                                                                          Indels
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AAG50369
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05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

08-APR-1999
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28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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19-APR-1999;
21-APR-1999;
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B-JUN-1999; B-JUN-1999; B-JUN-1999; B-JUN-1999;

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RESULT 12
AAG44031
ID AAG44
XX
AC AAG44
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                                                                                                                                 Query Match
Best Local Similarity 33...
Matches 10; Conservative
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33-CUT-1999
34-CUT-1999
35-CUT-1999
36-CUT-1999
37-CUT-1999
38-CUT-1999
39-CUT-1999
18-OCT-2000
               AAG44031;
                             AAG44031
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                              standard;
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(first entry)
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3-JUL-1999; 5-JUL-1999; 7-JUL-1999;

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PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 08/842
APPLICATION UMBER: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,44
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
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COMPUTER: IBM Compatil
                                                                                      REFERENCE/DOCKET NUMBER: 60
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TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF TH
NUMBER OF SEQUENCES: 33
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STREET: 100 Abbott
CITY: Abbott Park
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ZIP: 60064-3500
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100 Abbott Park Road
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KLASS, MICHAEL R.
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US-09-065-383-30
                                          ; MOLECULE TYPE: US-09-065-383-27
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TELEPHONE: 847/935-1729
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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APPLICATION NUMBER: US/09/065,383
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                           TOPOLOGY:
                                                                                         STRANDEDNESS:
                                                                                                                                                                                  TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                       LENGTH:
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 Similarity
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                                                                                                       amino acid
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                                                                                                                     518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
JENTION: REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIEDMAN, PAULA N. GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLPITTS, TRACEY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRANADOS,
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                                                           No. 6391543e
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Pred. No. 4.3e-23;
Score 215; DB 4;
Pred. No. 9.7e-22;
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              Length 518;
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; TYPE: PRT
; ORGANISM: IPIHb (IPP isomerase from Hevea brasiliensis)
US-09-296-754-2
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TYPE: PRT
; ORGALISM: Nicotiana tabacum
US-09-431-976-2
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                             RESULT 5
US-09-986-536-2
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US-09-296-754-2
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Sequence 2, Application US/09986536 Patent No. 6461841
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Korea Kumho Petrochemical Co. Ltd.
TITLE OF INVENTION: Isopentenyl diphosphate isomerase from Hevea Brasiliensis
FILE REFERENCE: PX99102/US
                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Applic
Patent No. 6316695
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Best Local
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                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/296,754A CURRENT FILING DATE: 1999-04-22 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Song, Wen TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase TITLE OF INVENTION: Expression FILE REFERENCE: 5051-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/021,286
PRIOR FILING DATE: 1998-02-10
PRIOR APPLICATION NUMBER: 60/049,471
PRIOR FILING DATE: 1997-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/431,976
CURRENT FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                                                                       SOFTWARE: KOPATIN 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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No. 642352
                                                                                               211 KWWENVENGTLKEAVDMKTIHKL 233
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                                                                                                                                  14 EWWENAGNKIYTMAAD-KTISKL 35
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                                                                                                                                                                   l Similarity
12; Conserv
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9; Conserv
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ilarity 52.9%;
Conservative
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52.28;
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Pred. No. 11
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; GENERAL INFORMATION:

APPLICANT: GEUEKE, BIRGIT

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APPLICANT: BOMMARIUS, ANDREAS
TITLE OF INVENTION: L-Amino Acid Oxidase from RP
FILE REFERENCE: 215209USOX
CURRENT APPLICATION NUMBER: US/09/986,536
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: DE 100 55 512.8
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 489
; TYPE: PRT
; ORGANISM: Rhodococcus opacus
US-09-986-536-2
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Query Match
Best Local Similarity
"hes 13; Conserva
                                                                           ; MOLECULE TYPE: protein US-08-793-229-35
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Best Local Similarity 35.6
Matches 16; Conservative
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                                                                                                                                                                                                     TELEFAX: (312)913-000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (312)913-0001
                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/793,229
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/0324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                             STRANDEDNESS:
                                                                                                                 TOPOLOGY:
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                                                                                                                                               : 528 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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QUAX, Wilhelmus Johannes
VENTION: Mutated Penicillin G Acylase Genes
                                                                                                                                                                                                                     (312)913-0002
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              Conservative
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                                                                                                                                 single
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35.6%;
                              23.7%;
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Pred. No. 37;
                            Score 51; DB
Pred. No. 47;
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                Mismatches
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                                            Length 528;
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RESULT 7
US-09-285-957-35
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; MOLECULE TYPE:
US-09-285-957-35
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US-08-469-486-52
                                                                                                                                                                                                Sequence 52, Application US/08469486 Patent No. 5739281
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Best Local Similarity
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                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Mutated Penicillin NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
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                                                            TITLE OF INVENTION: Improved method for the refolding TITLE OF INVENTION: proteins NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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ZIP: 60606
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                               STREET:
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                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                     355 EWWNNLHDKLFMDELGDFYGITKEITDHRYGASLAYKNISKESTNYK 401
                                                                                                                                                                                                                                                                                                                                       14 EWWENAGNKIY-----
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              Boston
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Massachusetts
                                 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 amino acids
                                                                                                                               Etzerodt,
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                Thoegersen, Hans Christian
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                                                 Fish & Richardson
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27.7%;
                                                                                                                                 Michael
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                        ----TMAADKTISKLMTEYK 40
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47;
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ATTORNEY/AGENT INFORMATION:

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Best Local Similarity 36.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          SOFTWARE: PatentIn Release #1.0, SOFTWARE: #1.25 CURRENT APPLICATION DATA:
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Th egersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION:
CLASSIFICATION:
                                                              CLASSIFICATION:
                                                                       APPLICATION NUMBER: US/08/469,658 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version SOFTWARE: #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                           OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 DPSRKKEWWENAGN--KIYTMAADKTISKLMTE 38
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5917018
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                                                                                                                                                                                                                                                                                          225 Franklin Street
                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                       Fish & Richardson
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February 4, 1994
N: 530
                                                                                                                                                                                                                                                                                                                                                          PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                        IMPROVED METHOD FOR THE REFOLDING OF
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Pred. No. 6.5e+
6; Mismatches
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                                                                                                                                            Version
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RESULT 11
US-08-673-789-5
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US-09-545-814-29
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US-09-545-814-29
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08673789 Patent No. 5814479
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LENGTH: 48
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Best Local
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/545,814 CURRENT FILING DATE: 2000-04-07
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SEQUENCE CHARACTERISTICS:
LENGTH: 4544 amino acids
                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                 NUMBER OF SEQUENCES:
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                              STREET:
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REGISTRATION NUMBER:
                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 EKKDPSRKK---EWWENAGNKIYTMAADK-----TISKLMTEYK 40
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NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09545814
                                                                                                                                                                                                                                                           ZHOU, RENPING; SCHULZ, NICHOLAS, T.; KROMER, LAWRENCE, F.; VANDE WOUDE, GEORGE, F.
                           345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                       MORGAN & FINNEGAN
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ER: 60/128,833
                                                                                                                                                METHODS
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                                                                                                                                                                        USE IN DIAGNOSTIC AND
                                                                                                                                                                                                                                      BSK RECEPTOR LIKE
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Pred. No. 50;
6; Mismatches
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Pred. No. 6.5e+02;
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RESULT 12
US-08-713-939A-79
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEFX: 421792
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                             FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Williamson, R. Anthony APPLICANT: Burton, Dennis R. TITLE OF INVENTION: ANTIBODIES SPINUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1:
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MEDIUM TYPE: FLOPPY
                               NAME: BOZÍCEVÍC, Karl
                                                                                                                                                                                                                                                                                                          STREET: 2200 Sand
CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
STRANDEDNESS: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                       APPLICATION NUMBER: FILING DATE: 13-SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
REGISTRATION NUMBER: 28, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                          94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), Application US/08713939A 5846533
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                                                                                                                                                                                                                                                                                                                                         2: Fish & Richardson P.C.
2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN
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                                                                                                                                                     US/08/713,939A
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                   28,807
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   06510/059001
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Pred. No. 1.2e+02;
5; Mismatches 8;
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   6 KKDPSRKKEW----WENAGNKIY-----TMAADKTISKLMTEYK 40
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US-09-036-579-79
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Query Match
Best Local S
Matches 14
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                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-854-5277
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/7
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/036,579 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                          TELEPHONE: 415-854-52
TELEFAX: 415-854-0875
                                                                                              TOPOLOGY: 1.i.
                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,807 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                      NAME: Bozicevic, Karl
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Local Similarity 29.8%;
es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                           ENGTH:
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ил. 6290954
глиатт
 l Similarity
14; Conserv
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                                                                                                                            amino acid
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                                                                                                                                             92 amino acids
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   Conservative
                                                                                              SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                               peptide
                29.8%;
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 Score 50; DB Pred. No. 7.8; 6; Mismatches
                                                                                                                                                                                                                                                         06510/059001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                               DB 4; Length 92;
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   15; Indels
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US-08-568-459A-13
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US-09-550-374-79
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                                                                                                                                                                Sequence 13, Application US/08568459A Patent No. 5849306
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
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                                                                                                             APPLICANT:
APPLICANT:
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APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
                APPLICANT: Su, Xin-zhaun APPLICANT: Wellems, Thoma TITLE OF INVENTION: BINDITITLE OF INVENTION: AND F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
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ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
   NUMBER OF
                                                                                  APPLICANT:
                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COmpatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/550,374
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10. 6372214
                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                          6 KKDPSRKKEW----WENAGNKIY-----TMAADKTISKLMTEYK 40
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 SEQUENCES:
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                                                                                             Chitnis, Chetan
Miller, Louis H.
                                                                                                                              Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                               Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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29.8%;
BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
37
                                               Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09/036,579
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                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 92;
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                                                                                                                                                                                                                                                                                                                          Indels
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; MOLECULE TYPE: PO
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: 11
; ORIGINAL SOURCE:
US-08-568-459A-13
Search completed: June 17, 2003, 12:03:40 Job time : 4.6896 secs
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                                                                                                                              Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                            Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0:
FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                 LENGTH: 291 amino acids
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                                                                                              5 EKKDPSRKKEWWENAGNKIYT 25
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                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                              Conservative
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                                                                                                                                           23.3%;
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                                                                                                                                           Score 50;
Pred. No.
                                                                                                                              Mismatches
                                                                                                                                                           DB
                                                                                                                                                           Length 291;
                                                                                                                              Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpaa/U;

2: /cgn2_6/ptodata/1/pubpaa/U;

3: /cgn2_6/ptodata/1/pubpaa/U;

4: /cgn2_6/ptodata/1/pubpaa/U;

5: /cgn2_6/ptodata/1/pubpaa/U;

6: /cgn2_6/ptodata/1/pubpaa/U;

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11: /cgn2_6/ptodata/1/pubpaa/U;

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12: /cgn2_6/ptodata/1/pubpaa/U;

13: /cgn2_6/ptodata/1/pubpaa/U;

14: /cgn2_6/ptodata/1/pubpaa/U;
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length: 2000000000
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         SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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9 US-10-077-040-1

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9 US-10-035-85-67

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9 US-10-123-904-90

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                  Sequence 11623, A
Sequence 11438, A
Sequence 350, Appli
Sequence 209, Appli
Sequence 106, App
Sequence 106, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 150, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 90, Appl
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      Query Match
Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11623
LENGTH: 388
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                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                    LENGTH: 388
TYPE: PRT
ORGANISM: Helicobacter pylor1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Trawick, John D.
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27.7%;
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Score 59.5; D
Pred. No. 9.1;
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; NAME/KEY: VARIANT
; LOCATION: (1)...(388)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-11458
                                                                                                                                                                                    US-09-881-752A-350
                                                                                                                                                   Sequence 350, Application US/09881752A Patent No. US20020115078A1
                                                                                                                                       GENERAL
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Best Local Similarity
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TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Encoding No. US20020115078Alel H TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 11458
LENGTH: 388
                                                                                                  APPLICANT:
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TYPE: PRT
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                    217 RLKLWWSNLQNSLFTLLPDRLANALRISDLPESYQ 251
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Zyskind, Judith
                                                                                 Miller, Charles
                                                  Comen,
                                                                                                  Al-Garawi,
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                                                                 Tomb, Jean-Francois
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                                                Raymond P.
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Best Local Similarity
Watches 12; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Nicotiana tabacum US-09-963-340-2
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TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-350
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Best Local :
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                                                                                                                                                                                                                                                Sequence 209, Application US/09712363 Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                            APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
TILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMERCE SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase TITLE OF INVENTION: Expression FILE REFERENCE: 5051-338
                                                              PRIOR APPLICATION NUMBER: PCT/US00/02246 PRIOR FILING DATE: 2000-01-28
                                                                                               CURRENT APPLICATION NUMBER: US/09/712,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 351
            APPLICATION NUMBER: 60/179,531 FILING DATE: 2000-02-01 APPLICATION NUMBER: 60/117,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Song, Wen
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Pred: No. 22;
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31;
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                                                                                                                                               AND
BY COMPARATIVE ANALYSIS
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FILING DATE:

APPLICATION NUMBER: 60/118,206

.999-02-

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: Sequence 4, Application US/10160293

Publication No. US20030022208A1

GENERAL INFORMATION:

APPLICANT: LINFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-050-704-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                    US-10-160-293-4
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US-09-712-363-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US200300
GENERAL INFORMATION:
APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,693
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/684,524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION: 62 Human Secreted Proteins FILE REFERENCE: P2039P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 462
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 231
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 60/134,092
FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/130,991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/165,124 FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 1999-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 APTVAGDDVFR--AWWDLAGNRAGPPSIARAVSKVIAE 214
                                                                                                                                                                                                            182 IRKKQPSSPLANTTYNIFIMDGKTWWHNSEEKNFTKLAKK 221
                                                                                                                                                                                                                                                     4 VEKKDPSRK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10050704
5. US20030050442A1
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Pred. No. 40;
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Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Indels
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; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-160-293-2
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; TYPE: PRT
; ORGANISM: Hun
US-10-160-293-4
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                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10077040 Patent No. US20020156014A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LINDQUIST, ETIKA et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOUI241-PROV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/160,293
CURRENT FILING DATE: 2002-06-04
NUMBER OF SEO ID NOS: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.28;
Local Similarity 32.68;
es 15; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 32.6 es 15; Conservative
                             ZIP: 94304

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
                 CURRENT
                                                                                                                                                                                                                                                        Patterson, Chandra
TITLE OF INVENTION: HUMAN NEUROSECRETORY PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KKDPSRKKEWWEN-AG---NKIYTMAA-----DKTISKLMT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KKDPSRKKEWWEN-AG---NKIYTMAA-----DKTISKLMT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                 CITY: Palo Alto
STATE: CA
APPLICATION NUMBER: US/10/077,040
                                                                                                                                               COUNTRY: USA
                 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              Corley, Neil C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.2%;
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Pred. No. 84;
8; Mismatches
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Pred. No.
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                                    2.0
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Publication

No. US20020192751A1

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; SEQ ID NO 150
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-150
               RESULT 11
US-10-036-041-67
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Best Local Similarity
Matches 15; Conserv
Sequence
                                                                                                                                                                       Best
                                                                                                                                                     Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No.
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/063,547 CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, E
                                                                                                                                                                                                                                                                                                    Prior Application removed - NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                       Local
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0510 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 254
67, Application US/10036041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150,
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                                                                                                                     6 KKDPSRKKEWWEN-AG---NKIYTMAA-----DKTISKLMT 37
                                                                                                                                                     l Similarity 32.6
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 468 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                  EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: ISLTNOT01
CLONE: 2379427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                    Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                Grimaldi, Christopher J.
Gurney, Austin L.
Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filvaroff, Ellen
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p. US20020182638A1
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                                                                                                                                                                   24.28;
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                                                                                                                                                  Score 52; DB 9;
Pred. No. 1e+02;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 9;
Pred. No. 1e+02;
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GENERAL
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APPLICATION NUMBER: 60/112514
FILING DAME: 1998-05-15
          APPLICATION NUMBER: 60/J
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/130359 FILING DATE: 1999-04-21
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                                                                                                  APPLICATION NUMBER: 60/144791
                                                                                                                                       APPLICATION NUMBER: 60/138166
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APPLICATION NUMBER: 09/311832
                                                  FILING DATE:
                                                                     APPLICATION NUMBER: 60/146970
                                                                                                                     FILING DATE: 1999-06-08
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                                                                                       FILING DATE: 1999-07-20
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LLING DATE: 1999-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
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Gurney, Austin L.
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe, Colin Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A.
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RESULT 12
US-10-028-072-90
; Sequence 90, Application US/10028072
; Publication No. US/20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: HOMO
US-10-036-041-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NI
PRIOR FILING DATE:
NUMBER OF SEQ ID NO
SEQ ID NO 67
LENGTH: 468
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Best Local S
Matches 15
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FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US00/14042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US00/05601 FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/908,827 FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/869599 FILING DATE: 2001-06-29
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| Similarity 32.68;
| Similarity 32.68;
                                                                                                                                                                                                         EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 254
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2001-06-20
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Pred. No. 1e+C
8; Mismatches
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1e+02;
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CURRENT FILING DATE: 2001-12-19
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                  OR APPLICATION NUMBER: 60/06285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06287
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/062814
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063329
OR APPLICATION NUMBER: 60/063329
OR APPLICATION NUMBER: 60/063329
OR APPLICATION NUMBER: 60/063329
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063733
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OR APPLICATION NUMBER: 60/063735
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DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059263
DR FILING DATE: 1997-09-18
DR APPLICATION NUMBER: 60/059352
DR FILING DATE: 1997-09-19
DR APPLICATION NUMBER: 60/059588
DR APPLICATION NUMBER: 60/059588
DR FILING DATE: 1997-09-19
DR FILING DATE: 1997-09-19
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OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059115
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059117
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Filvaroff, Ellen
Gao, Wei-Qiang
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Watanabe, Colin K
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RESULT 13
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; Publication No. US2003
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; APPLICANT: Godowski,
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                                     Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
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FILING DATE: 1998-02-04
APPLICATION NUMBER: 60/074086
FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/074092
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APPLICATION NUMBER: 60/077791 FILING DATE: 1998-03-12 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294

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FILING DATE: 1998-01-23
APPLICATION NUMBER: 60/073617
FILING DATE: 170

APPLICATION NUMBER: 60/0 FILING DATE: 1997-12-16 FILING DATE: 1997-12-11

60/069694 60/069334 60/069278 60/069212

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60/066770

60/066511

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APPLICATION NUMBER: 60/066453 FILING DATE: 1997-11-24

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NUMBER: 6: 1997-10-

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NUMBER:

1997-11-

APPLICATION NUMBER: 60/065186 FILING DATE: 1997-11-12

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Stewart, Timothy A. Watanabe, Colin K. Wood, William I.
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FILING DATE: 1998-04-24
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/129122
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 APPLICATION NUMBER: 09/854208
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                                                                                                                                                                             EEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLT 254
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                                                                     Eaton, Dan L.
            Goddard, Audrey
Godowski, Paul J.
                                      Gerritsen, Mary
Grimaldi, Christopher
                                                      Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE
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                                                                                              Application US/10063616
b. US20030013855A1
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                                                                                                                                                                                                                                                                                                    Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: PCT/US01/06520: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER: PCT/US00/34956
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Pred. No.
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Gurney, Austin L. Watanabe, Colin K.

Wood, William I

POLYPEPTIDES AND NUCLEIC

NUMBER: US/10/063,616

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FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NO 150
LENGTH: 468
TYPE: PAT
ORGANISM: Homo Sapien
US-10-063-502-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CURRENT FILING DATE: 2002-05-03; Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 170; SEQ ID NO 150; LENGTH: 468; TYPE: PAT ORGANISM: Homo Sapien
US-10-063-616-150
Search completed: June 17, 2003, 12:02:31 Job time: 5.27526 secs
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US-10-063-502-150
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Best Local Similarity 32.6%;
Matches 15; Conservative
                                                                                                                                  Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 150, Application US/10063502
Publication No. US20030023042A1
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                 TILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TILE OF INVENTION: ACIDS ENCODING THE SAME THE REFERENCE: P3230R1C1
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                                                                                      Grimaldi,Christopher J.
Gurney,Austin L.
Watanabe,Colin K.
Wood,William I.
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Godowski, Paul J.
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Gerritsen, Mary E.
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illarity 32.6%;
Conservative
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Pred. No. 1e+02;
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Pred. No. 1e+02;
B; Mismatches
                                                                                                                                    9;
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Scoring table:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A;Dethway: xylan degradation
C;Superfamily: Pseudomonas endo-1,4-beta-xylanase F; Streptomyces endo-1,4-beta-xylan
C;Superfamily: Pseudomonas endo-1,4-beta-xylanase F; Streptomyces endo-1,4-beta-xylanase
F;1-19/Domain: signal sequence *status predicted <SIG>F;20-621/Product: endo-1,4-beta-xylanase B *status predicted <MAT>
F;302-615/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
F;403,516/Active site: Glu *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
S59632
    A;ACCESSION: 14161
A;ASCESSION: 14161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-604 <SEE>
A;Cross-references: EMBL:AL031545; PIDN:CAA20842.1; GSPDB:GN00068; SPDB:SPCC285.03
A;Cross-reference: strain 972h-; cosmid c285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Cellvibrio mixtus C;Speckes: Cellvibrio mixtus C;Date: 15-Feb-1996 #sequence_revision 11-Apr-1997 #text_change 18-Jun-1999 C;Accession: S59632; S52742 R;Millward-Sadler, S.J.; Davidson, K.; Hazlewood, G.P.; Black, G.W.; Gilbert, H.J.; C Biochem. J. 312, 39-48, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-621 <MIL>
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A; Experimental C; Genetics:
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Result No.

18 19 20 20 21 22 23 24 25 27 28

14 15 16

11 12 13

Mismatches

16;

Indels

0

Gaps

0

38

DB 1;

Length 621

fission yeast (Schizosaccharomyces pombe)

#text\_change 17-Nov-2000

Barrell, B.G

Minimum DB Maximum DB

Database

Searched:

ALIGNMENTS

Sequence:

Title:

on:

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C;Genetics:
A;Gene: rodA_2
C;Superfamily: rod shape-determining protein
                                                                                                                                                                                                                                                                    R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and E A;Reference number: A97359; PMID:11743194
A;Accession: G98202
                                                                                                                                                                                                                                                                                                                                                                        C;Species: Agrobacterium tumefaciens (stra C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: G98202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable rod shape-determining protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: D71804
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R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, (Nature 397, 176-180, 1999)
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A; Map position: 3
C; Superfamily: fruit fl
                                                                                                                                                        A; Map
                                                                                                                                                                                                                                                                                                                                                                                                          probable oxidoreductase PA4167 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
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A; Residues: 1-388 <ARN>
A; Cross-references: GB:AE001568; GB:AE001439; NID:g4156083; PIDN:AAD07042.1;
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A; Residues: 1-277 <KUR>
                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                     Query Match
Best Local
                                                                                                                                        Superfamily: aldehyde
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14; Conservative
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   KVWVENYGHDAFIKSVDESLKKLKTDY 98
                                  KEWWENAGNKIYTMAADKTISKLMTEY 39
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37.0%;
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Pred. No. 4.
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Pred. No. 8
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                                                                                                     Length 277;
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kelz, B.;
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                             C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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C;Accession: AE1698
R;Glaser, P.; Frangeul, L.;
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Duchaud,

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he, P.; K.D.; !

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Buchrieser, C.;

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- Listeria

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(strain

Clip11262)

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C;Accession: A69407

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, P.; R;Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Ki.; Fleischmann, R.D.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Nature 390, 364-370, 1997

Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                   A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69407
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signal recognition particle, subunit SRP19 (srp19) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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A;Map position: linear chromosome
C;Superfamily: aldehyde reductase
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A;Title: The Genome of the Natural Genetic
A:Reference number: AB2577; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB3084
                                                                                                                                                                            A;Cross-references: GB:AE001017; GB:AE000782; C;Superfamily: conserved hypothetical protein
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-104 <KLE>
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A; Residues: 1-277 <KUR>
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15; Conserv
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10; Conser
EKKYP---KSWWEEGGRVVVEKRGTKT--KLMIE
                                           EKKDPSRKKEWWENAGNKIYTMAADKTISKLMTE 38
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                                                                                                         27.28;
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                                                                                      Score 58.5; I
Pred. No. 2.8;
1; Mismatches
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Pred. No. 6.
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6.7;
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M.; McCl
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H85806

Hypothetical protein 22984 [imported] - Escherichia coli (strain 0157:H7, shypothetical protein 22984 [imported] - Escherichia coli (strain 0157:H7, sc;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85806
A;Status: preliminary
A;Molecula type: DNA
A;Residues: 1-201 <STO>
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; A;Ittle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1698
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-921 <GLA>
A;Residues: 1-921 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97357.1; PID:g16414641; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: ileS
C;Superfamily: isoleucine-tRNA ligase
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90958
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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A;Cross-references: GB:BA000007; PIDN:BAB36061.1; PID:g13362106; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2638
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: F90958
C;Accession: F90958
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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Pred. No. 36;
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No. 7
                                                                                                                                                                                                                                                                                                                       Escherichia coli (strain O157:H7, substrain
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                                                                                                                                                                                     J.D.; Rose,
Potamousis,
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Voss, H.; W
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                                                                                                                                                                                  D.J.;
K.; Aj
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Wehland,
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A; Map position: 2

C; Superfamily: tartrate-resistant acid phosphatase; phosphoesterase C; Keywords: iron; metalloprotein; phosphoric monoester hydrolase F;1-21/Domain: signal sequence #status predicted <SIG>F;22-304/Product: acid phosphatase #status predicted <MAT>F;22-121/Domain: phosphoesterase core homology <PEC>F;42-121/Domain: phosphoesterase core homology <PEC>F;48,81,84,26/Bhinding site: iron (Asp. Asp. Tyr. His) #status prediff;81,119,189,224/Binding site: iron (Asp. Asn. His, His) #status prediff;81,119,189,224/Binding site: prodicted figure for the first fir
                                                                                                                                                                                                                                                                                                                               A;Cross-references:
C;Genetics:
A;Gene: At2g01880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable acid phosphatase (EC 3.1.3.2) At2g01880 N;Alternate names: purple acid phosphatase C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-200 C;Accession: C84430
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A; Residues: 1-388 <TOM>
A; Cross-references: GB:/
C; Superfamily: rod shape
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Reference number: A64520; MUID:97394467; PMID:9252185
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-304 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: C84430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Date: 09-Aug-1997 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE002093; NID:g4522007; PIDN:AAD21780.1;
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Score 56;

DB

1;

Length

304;

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probable membrane protein YGL075c - N;Alternate names: hypothetical prot C;Species: Saccharomyces cerevisiae C;Date: 17-May-1996 #sequence_revisiC;Accession: S64082
                                                                                                     RESULT 14
S64082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
T02232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein BYJ6 - common tobacco (fragment)
C;Species: Nicotiana +ahaarr '--
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T02232
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Imanishi, S.; Hashizume, K.; Nakakita, M.; Kojima, H.; Matsubayashi, Y.; Hashimoto, T Plant Mol. Biol. 38, 1101-1111, 1998
A;Title: Differential induction by methyl jasmonate of genes encoding ornithine decarbo; A;Reference number: Z14631; MUID:99084761; PMID:9869416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
C;Accession: T02232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Genetic code:
C; Superfamily: s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Tille: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: $73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal recognition particle protein ffh - Mycoplasma pneumoniae (strain ATCC 29342) N.Alternate names: hypothetical protein D09_orf450
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; PIDN:AAB95741.1; PID:g16737
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA .
A; Residues: 1-450 <HIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: S73419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Himmelreich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date:
                    Best
                                                                                                                                                                                                                                                                                                                                  Cross-references: EMBL:AB005879; NID:g2280519; PIDN:BAA21616.1; Experimental source: Strain Bright Yellow 2
                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-177 <IMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999 sion: S73419
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13; Conser
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10; Conser
                                                                                                                                                                                                                                                            Similarity
9; Conser
                                                                                                                                                                                 DPSLKVEWYVNDGDKVH
                                                                                                                                                                                                                      DPSRKKEWWENAGNKIY 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEY 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSLQKQWYSVLGNHDYRGNVEAQLSKVLTQ 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      larity 33.3%;
Conservative
                                                         protein YGL075c - yeast (Saccharomyces hypothetical protein G3219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.0%;
                                                                                                                                                                                                                                                                             25.6%;
                                                                                                                                                                                 166
                                                                                                                                                                                                                                                          Score 55; DB
Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 18;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 27;
); Mismatches
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27;
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                                                                                 cerevisiae)
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C:Keywords: hydrolase; phosphoprotein
F:39-56/Domain: calcium binding #status predicted <CAI>F:106-130/Domain: calcium binding #status predicted <CAI
F:236-256/Domain: calcium binding #status predicted <CAI
F:317-336/Domain: calcium binding #status predicted <CAI
F:317-336/Domain: calcium binding #status predicted <CAI
F:317-336/Domain: ATP binding #status predicted <ATP>
F:610-784/Domain: ATPase nucleotide-binding domain homol
F:755-776/Domain: calcium binding #status predicted <CAI
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T04172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-Apr-2002
C;Accession: T04172
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C; Superfamily: Saccharomyces cerevisiae
C; Keywords: transmembrane protein
F;311-327/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-387 <RIE>
A; Cross-references: EMBL: Z72597;
20
                                                                                                          F;755-776/Domain: calcium pinging *status predicted F;358/Active site: Asp (aspartylphosphate intermediate) *status predicted
                                                                                                                                                                                                                                                                                                                            C; Superfamily: Na+/K+-transporting ATPase alpha
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1048 <CHE>
A;Cross-references: EMBL:U82966; NID:g2160711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant J. 11, 363-371, 1997
A;Tille: Cloning of a Ca(2+)-ATPase gene and the role of A;Reference number: Z15255; MUID:97260952; PMID:9107028
A;Accession: T04172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ca2+-transporting ATPase (EC 3.6.3.8) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, submitted to the Protein Sequence Database, May 1996 A;Reference number: S64071 A;Accession: S64082
                                                                                                                                                                                                                                                                                                                                                    A; Introns: 444/3; 521/3; 615/3; 729/3; 779/3; 854/3
                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Chen, X.; Chang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: SGD:S0003043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SGD: MPS2; MIPS: YGL075c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source:
                                               Matches
                                                                                     Query Match
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  14 EWWENAGNKIYTMAADKT
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                                             Conservative
                                                                                                                                                                         ATP binding #status predicted <ATP>
ATPase nucleotide-binding domain homology
                                                                                                                                                                                                                    calcium binding #status predicted <CA3> calcium binding #status predicted <CA4>
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                                                                                                                                                                                                                                                                                                                                                                                                  cv.IR36
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46.4%;
                                                                 25.1%;
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S288C
  31
                                                                 Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54;
Pred. No.
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                                                                 1.1e+02;
                                                                                   BB
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                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                chain; ATPase
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                                             6,
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                                                                                                                                                                                                                                                                                                                                nucleotide-binding
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1 SPKVEKKDPSRKKEY
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YGH5_YEAST
PPCK_DEIRA
SECA_PORPU
Y130_METJA
STS4_MYCGE
SYL_BORBU
ATX1_PLAFA
APR16_ARATH
ORPB_HUMAN
MATA_BACSH
Y771_METJA
BX42_DROME
YE37_MYCPN
AOR_PYRFU
PAC_ARTVI
YEEJ_ECOS7
LRP1_CHOCN
LRP1_HUMAN
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6 human papil
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9 equine infe
plasmodium
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7 borrelia bu
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Peptidoglycan synthesis; Cell wall; Cell division; Cell shape;
Transmembrane; Inner membrane; Complete proteome.
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	Q07497 gallus gall P28693 gallus gall	Q92180 bos taurus Q07498 gallus gall				Q09336 caenorhabd1		P76347 escherichia		002626 caenorhabdi

## ALIGNMENTS

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H	2001 (Rel.
H	16-OCT-2001 (Rel. 40, Last sequence update)
Ţ	16-OCT-2001 (Rel. 40, Last annotation update)
Ħ	Probable cell division protein ftsw.
z	FTSW OR JHP1468.
S	Helicobacter pylori J99 (Campylobacter pylori J99).
ი	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Ç	
×	NCBI_TaxID=85963;
z	[1]
Ъ	SEQUENCE FROM N.A.
> ×	MEDLINE=99120557; PubMed=9923682;
>	Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
⋗	Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Þ	Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
A	Trust T.J.;
н	"Genomic sequence comparison of two unrelated isolates of the human
· <del>3</del>	gastric pathogen Helicobacter pylori.";
-	Nature 397:176-180(1999).
· C	-!- FUNCTION: THIS IS A SEPTUM-PEPTIDOGLYCAN BIOSYNTHETIC PROTEIN,
0	INVOLVED IN CELL WALL FORMATION. PLAYS A ROLE IN THE STABILIZATION
3 (	
) C	- i- SUBCELLULAR LOCATION: Integral membrane protein, inner membrane
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n c	- CARACTERISTIC CONTROL OF A CO
O.	This SWISS-PROT entry is copyright. It is produced through a collaboration
a	between the Swiss Institute of Bioinformatics and the EMBL outstation -
ဂ	the European Bioinformatics Institute. There are no restrictions on its
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C	or send an email to license@isb-sib.ch).
a	
×	EMBL; AE001568; AAD07042.1;
מינ	InterPro; IPR001182; Cell_cycle.
×	Plam; Prologe; FTSW_RODA_SPOVE; 1.

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RESULT
SR19_A
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhulyan S.H., Gowda K., Hotokezaka H., Zwassembly of archaeal signal recognition components.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Courselbush J., Lee N.H., Sutton G.G., Gill S. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zh. Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                             recognition particle.";
Biochemistry 39:12862-12874(2000)
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MEDLINE-20150251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
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MEDLINE-20496765; PubMed-11041851;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mener J.L., Wilson C.;
Role of SRP19 in assembly of the Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loca 1
                                                                                                                                                                                                                                                             SRP19.
- SUBCELLULAR
- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY, BINDS DIRECTLY TO 7S RNA AND MEDIATES BINDING OF THE 54 KDA SUBUNIT OF THE SR SUBUNIT: ARCHAEAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S MOLECULE OF 300 NUCLEOTIDES AND TWO PROTEIN SUBUNITS: SRP54 AND T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217
AE001017; AAB89988.1; AF1258; -.
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                                                                requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                      pylori.",
nature 388:539-547(1997).
-I- FUNCTION: THIS IS A SEPTUM-PEPTIDOGLYCAN BIOSYNTHETIC INVOLVED IN CELL WALL FORNATION. PLAYS A ROLE IN THE S
OF THE FTSZ RING DURING CELL DIVISION (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Integral membrane protein. Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-26695 / ATCC 700392;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F. White O. Kerlavage A
Fleischmann R.D., Ketchum K.A., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD006609; SRP19; 1.
Signal recognition particle; RNA-binding; Ribonucleoprotein;
Complete proteome.
SEQUENCE 104 AA; 12405 MW; 72D5DDABB4E89E64 CRC64;
                                                                                                                                                              EMBL; AE000654; AAD08600.1; -. TIGR; HP1560; -.
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                                                                                          Transmembrane;
                                                                                                       Peptidoglycan synthesis;
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                                                                                                                                      Pfam; PF01098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter.
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                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                               (By similarity). SIMILARITY: BELONGS TO THE FTSW/RODA/SPOVE FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                           complete, genome sequence
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oteobacteria; epsilon subdivision;
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P75054;
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SEQUENCE
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-I- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE RIBOSOMES (BY SIMILARITY).

-I- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH (BY SIMILARITY).

-I- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                        Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                   InterPro: IPR000897: SRP54.
InterPro: IPR004125: SRP54_SPB.
InterPro: IPR004780: SRP_sub.
                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000011; AAB95741.1; HSSP; O07347; 1FFH.
                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma pneumoniae. Bacteria; Firmicutes;
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FFH OR MPN061 OR MP093.
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01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
                                                                                                                        Complete
                                                                                                                                              Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long if it is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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rticle protein (Fifty-four
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Pred. No. 7
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OS Saccha
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37 kDa cell
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                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                          Sentandreu M., Elorza M.V., Valentin "Cloning of cDNAs coding for Candida". Med. Vet. Mycol. 33:105-111(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of CSP37, putative membrane protein of Candida al J. Bacteriol. 179:4654-4663(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 26555;
MEDLINE-97386400; PubMed-9244249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic NCBI_TaxID=5476;
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 188-321 FROM N.A. STRAIN-ATCC 26555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sentandreu M., Nieto A.,
Fonzi W.A., Sentandreu R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans (Yeast).
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  Saccharomyces
                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                            EMBL; U89676;
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SUBCELLULAR LOCATION: Cell wall.
                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                       wall.
                                                                                                                           137
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Pred. No.
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Best Local :
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16-OCT-2001
16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                         Science 286:1571-1577(1999).
Science 286:ACTIVITY: ATP + oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20036896; PubMed-10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.I. Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L. Haft D.H., Jiang L., Pamphile W., Crosby M., Shen M., Woffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathavan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann F. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long-as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoenolpyruvate Carboxykinase [ATP] (EC 4.1.1.49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97435481; PubMed=9290212; Rieger M., Brueckner M., Schaefer M., "Sequence analysis of 203 kilobases f:
                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                           Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deinococcaceae;
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carboxykinase) (Phosphoenolpyruvate
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                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                          + CU(2).
PATHWAY: Rate-limiting gluconeogenic enzyme.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
STMTLARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CA
        European
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13; Conserv
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387 AA; 44585 MW; CF8AF
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46.4%;
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        Institute.
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        restrictions
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Query Match Best Local S Matches 16

Similarity 16; Conserv

Conservative

9,

Mismatches

7;

Indels

25;

Gaps

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Pred. Score 53.5;

No.

39;

DΒ

Length

24.9%; 28.1%;

SEQUENCE

884 AA;

101325 MW;

A415846D12B90B2B

(BY SIMILARITY)

Translocation;

Protein transport; NP\_BIND 98

PROSITE;

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RESULT 8
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ID SECA_P
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OC EUKARY
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P51381;
01-OCT-1996
01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00532; PEPCK_ATP; 1.

Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete NP_BIND 237 244 ATP (BY SIMILARITY).
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Reith M.E., Munholland
                                                                                                                                        InterPro; IPR000185; Seca.
Pfam; PF01043; Seca_protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
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                                                                                          TIGRFAMS; TIGRO0963; secA; 1.
                                                                                                                                                                                     EMBL; U38804; AAC08267.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                              CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO PRE-SECRETORY PROTEINS ACROSS THE MEMBRANE.
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE SECA FAMILY.
                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation accordant to the Swiss Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE001950;
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                                                                                                                     PR00906;
                            rs01312; SECA; 1.
transport; ATP-binding; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPKDRFIVEDDQTRETVWWEGFNQPISAEVFDRLLDKMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPK---VEKKDPSRKKEWWENAGNKIYTMAADKTISKLM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translocase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 AA;
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                                                                                                                                          SecA_protein;
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                                                                                                                     SECA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34, Created)34, Last sequence up35, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.;
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53.5;
Pred. No. 20;
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                                                                                      Query Match
Best Local
                                                                      Matches
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschil.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: STRONG, TO M.JANNASCHI MJ1218 AND MJ1531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y130_METJA
Q57594;
                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                              Hypothetical
                                                                                                                                                                         InterPro; IPR000055; Methylase_S. Pfam; PF01420; Methylase_S; 2
                                                                                                                                                                                                            EMBL; U67470; AAB98112.1; -.
TIGR; MJ0130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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 245
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                                   9
                                                                                      Similarity
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PSTKKSEYWENGEINWITPLDLSRLNEKIYIGSSERKVTKIALE 288
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                                 PSRKK-EWWENA---
                                                                                                                                        11 protein: Complete proteome.
343 AA; 39061 MW; 5184D68686274603 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 35, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein MJ0130.
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                                                                                    24.7%;
29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -WENAGNKIY-----
                                                                    Score 53; DB
Pred. No. 17;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                 -GNKIYTMAADKTISKLMTE 38
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                                                                      9;
                                                                                                       Length 343
                                                                    Indels
                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.D.,
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450
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                                                         Matches
                                                                       Query Match
Best Local
                                                                                                                                                                                                                                            InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
InterPro; IPR004780; SRP_Sub.
Pfam; PF00448; SRP54; 1.
Pfam; PF02081; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
PTGRPAMS; TIGR00959; 3a0501s01; 1
                                                                                                               NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Eleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal recogn
FFH OR MG048
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39684; HSSP; 007347;
                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SR54_MYCGE
P47294;
                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                       Complete
                                                                                                                                                                                                                  Signal recognition particle;
                                                                                                                                                                                                                                 PROSITE; PS00300; SRP54;
                                                                                                                                                                                                                                                                                                                                                                TIGR; MG048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma
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                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH (BY SIMILARITY). DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
387
                                                       Similarity
12; Conser
                                                                                                                                                                                                    proceome.
PKLINRDPNRKQRIIKGSGRKM----
                           PKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEY
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                                                                                                                 446
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                                                                                                                                            294
106
188
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                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33, Last sequence update)
40, Last annotation update)
n particle protein (Fifty-four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33, Created)
                                                                                                                                              293
446
113
192
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                                                                                                               50199
                                                                     24.7%;
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                                                         10;
                                                                                                                             G-DOMAIN.
M-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                  GTP-binding; RNA-binding;
                                                                       Pred.
                                                                                   Score 53;
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                                                                                                                  080F2255C8B5E5AE
                                                         Mismatches
                                                                       ŏ.
-- DELNKLMKEW
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23;
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                                                         Indels
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SYL_BORBU

ID SYL_B
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ATX1_PLAFA
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Best Local S
Matches 13
                 ATX1_PLAFA
Q04956;
30-MAY-2000
30-MAY-2000
16-OCT-2001
Probable cat
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Leucyl-tRNA sy:
LEUS OR BB0251
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BINDING
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entitles requires a license agreement (Se
or send an email to license@isb-sib.ch).
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002302; Leu-tRNAsynt
InterPro; IPR002300; tRNA-synt_la
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001135; AAB91495.1; TIGR; BB0251; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic sequence of a Lyme disease spirochaete, burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garland S., Fujii C., C
Smith H.O., Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; (
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30-MAY-2000
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                        l Similarity
13; Conserv
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               000 (Rel. 39, Created)
000 (Rel. 39, Last sequence update)
001 (Rel. 40, Last annotation update)
cation transporting ATPase 1 (EC 3.6.3.-).
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falciparum
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                                                                                                                             STANDARD;
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tRNA-synt_la.
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annotation update)
6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
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                                                                                                                                                                                                                                                                                                                                                                                                       "KMSKS" REGION.
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                 Length 840;
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RESULT 13
PP16\_ARATH
ID PP16\_A
AC P48486
DT 01-FEB
DT 01-FEB
DT 16-OCT

PP16\_ARATH S
P48486; Q9SUT7;
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01-FEB-1996 (Rel
16-OCT-2001 (Rel

5 (Rel. 33, 5 (Rel. 33, 1 (Rel. 40,

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Last sequence update)

STANDARD;

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Best Local :
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TRANSMEM
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J. Cell Biol. 120:385-398(1993).
J. Cell Biol. 120:3
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1074
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                                   N
                                                                         . Similarity
12; Conserv
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PVVGKNNKQKKKLVWYNHKNDTYLKGHDKT
                                   PKVEKKDPSRKKEWWENAGNKIYTMAADKT
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1760
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G., Meade J.C.,
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                                                                                         24.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation;
                                                                                                                                                    MW;
                                                                         2;
                                                                       Score 52; DB 1;
Pred. No. 1.4e+02;
2; Mismatches 16
                                                                                                                                                                                                                                                                   MAGNESIUM
POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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                                   31
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                                                                                                              Length 1956;
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                                                                         0;
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RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Accaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schon M., Strontey L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Pulton B., Miller N., Gereco T., Kemp K.,
RA Kramer J., Filton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Minx P., Bentley D., The Schutz K., Drone K., Cotton M., Johnson C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Granat S., Shohdy N., Haseawa A., Hameed A., Lodhi M., Johnson A.,
RA Granat S., Shohdy N., Haseawa A., Hameed A., Lodhi M., Johnson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H
De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
Van Montagu M., Rogers J., Cronin A., Ouall M., Bray-Allen S.,
Van Montagu M., Rogers J., Cronin A., Ouall M., Bray-Allen S.,
Van Montagu M., Rogers J., Cronin A., Ouall M., Bray-Allen S.,
                                        Granat S., Shohdy N., Hasegawa A., Hameed A., Lod
Chen E., Marra M., Martienssen R., McCombie W.R.;
"Servence and analysis of chromosome 4 of the pla
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Pohl T
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin Q., Li J., Smith R.D., Walker J.C.;
"Molecular cloning and chromosomal mapping of type one serine/threonine protein phosphatases in Arabidopsis the Plant Mol. Biol. 37:471-481(1998).
                    "Sequence and thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.
Welchselgartner M., de Simone V., Obermaier B., Mache R.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20083488; PubMed=10617198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95291339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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TOPP6 OR PP1BG OR AT4G11240 OR F8L21.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel Arabidopsis type 1 protein phosphatase is highly expressed male and female tissues and functionally complements a conditional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ale and female tissues and func
cycle mutant of Aspergillus.";
t J. 7:823-834(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columbia;
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Entian K.-D., Terryn N.,
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                                                                                          Johnson
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Best Local
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15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Oxysterol binding protein-related prot
(ORP-11)
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ACT_SITE
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METAL
METAL
                                                                          SEQUENCE FROM N.A.
MEDLINE-21601154; PubMed-11735225;
Jaworski C.J., Moreira E., Li A., Lee
"A family of 12 human genes containing
Genomics 78:185-196(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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EMBL; U80921; AAC39460.1; --
EMBL; AL096882; CAB51408.1;
EMBL; AL161531; CAB81225.1;
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                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                            ORPB_HUMAN
Q9BXB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0114; STPHPHTASE. ProDom; PD000252; S/T_phosphtse; SMART; SM00156; PP2AC; 1.
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                                          SEQUENCE OF 1-315
                                                                                                                                                                                                                                                                             OSBPL11 OR ORP11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08129; 1FJM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                      MEDLINE-21376257;
                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
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TISSUE SPECIFICITY: STRONGLY UPREGULATED FLOWERS, ESPECIALLY IN THE TAPETUM, THE I POLLEN AND IN THE OVARIES.

STMITARITY: BELONGS TO THE PPP FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
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13; Conser
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    Laitinen
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  PubMed=11483621;
n S., Chinetti G.,
                                          FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                  Chordata;
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41.9%;
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Pred. No. 25;
2; Mismatches
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IRON (BY SIMILARITY).

IRON (BY SIMILARITY).

IRON AND MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

GENERAL ACID (BY SIMILARITY).
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MANGANESE (BY SIMILARITY).
D -> V (IN REF. 3).
GGKGR -> V (IN REF. 3).
                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                 tion update)
protein 11
                                                                                                                                                                                                                                                                                                                                                       update)
    Johansson
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                                                                                                 R., Rodriguez I.R. g oxysterol-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992
01-AUG-1992
01-OCT-1996
                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staels B., Ikonen E., Olkkonen V.M.;
"The OSBP-related protein family in humans.";
J. Lipid Res. 42:1203-1213(2001).
-I- TISSUE SPECIFICITY: Widely expressed.
-I- SIMILARITY: BELONGS TO THE OSBP FAMILY.
-I- SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00169; PH; 1.
Pfam; PF01237; Oxysterol_BP; 1.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-87083389; PubMed=3025178;
                                                                                                                                                                                                                                                                                                                                                                                 Bacillus sphaericus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1421;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Probable macrolide acetyltransferase (EC 2.3.1.-) (Fragment).
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PROSITE; PS50003; PH_DOMAIN; 1.
Lipid transport; Transport.
DOMAIN 58 155 PH.
                             EMBL; M15332; AAA22417.1; ALT_INIT
HSSP; P26841; 2XAT
                                                                                                                                                                                                                                                                 Bacillus sphaericus.";
                                                                                                                                                                                                                                                                                   macrolide-lincosamide-streptogramin B resistance element from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                  Monod M., Mohan S., Dubnau D.;
"Cloning and analysis of ermG, a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATA_BACSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                            Bacteriol. 169:340-350(1987).
- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 LEKODPFESRRLWKNVTDSLRESEIDKA----TEHK 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:16397; OSBPL11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001849;
            IPR001451; Hexapep_transf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
hexapep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 51.5; DB; Pred. No. 59; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B443D3BDE8AE5FB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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Ър
                                                                                                              SQ SQ
                                                       Matches
                                                                     Query Match
Best Local
                                                                                                           PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Antibiotic resistance; Transferase; Acyltr
NON_TER 1 1
SEQUENCE 180 AA; 20399 MW; 7EDF56157EF
135 EKIEFLLKLEWWNWSGEEIFDNLEILTSEAGLEELMNKY 173
                         5 EKKDPSRKKEWWENAGNKIY----TMAADKTISKLMTEY 39
                                                      l Similarity
11; Conser
                                                      Conservative
                                                                    23.7%;
28.2%;
                                                                                                                                        Transferase; Acyltransferase; Repeat.
                                                      10;
                                                                  Score 51;
Pred. No. :
                                                                                                              7EDF56157EF63B1A CRC64;
                                                      Mismatches
                                                                    DB 1; Length 180; 16;
                                                    14; Indels
                                                                  į,
                                                       4.
                                                      Gaps
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1;

Search completed: June 17, 2003, 11:56:48 Job time: 3.40117 secs

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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
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                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq
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length: 2000000000
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180
1 SFQSESSTPSTGGF
 100.0
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32.8
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461.981 Million cell updates/sec
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Gapop 10.0 ,
                                                                                                                                            Match
                                                                                                                                                        Query
                                                                                                                                                                                                                                                                A_Geneseq_101002:*
1: /SIDS2/gcgdata/c
2: /SIDS2/gcgdata/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                          SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199, DAT:

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199, DAT:

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000, DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                            Length
                        518
518
1807
1982
1061
253
1403
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 19
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AAM50811
AAW85472
AAM85472
AAM69728
ABG09731
ABG09731
ABB59318
ABG05957
ABB60540
AAU42806
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                     PS118 prostate mar
PS118 protein enco
PS118 prostate mar
Novel human diagno
Novel human diagno
Drosophila melanog
Novel human diagno
                                                                                                                                          Description
Propionibacterium
Drosophila melanog
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                                                                                                                                                                                                                                      have
                                                                                                                                                                                                                       printed,
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AAM50811
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2.5	N	2.5 2	2.5 2	5 2	5 .	3 2	5 2	5 2	5 2	5 2	. 3	3	3	5 3	5 3	5 3	<b>5</b> 3	5 3	ω	<b>5</b>	<b>υ</b>	5 3	5 3	5 3	5 3	6 3	6 3	6 3	6 3	6 3	6 3	56 3	6 3	σ
	. 9	.9	9	9.	9	9	9.	9.7	9.7	9.7	0.0	0.0	0.0	0.3	0.3	0.3	0.3	0.3	0.ω	0.3	ο. ω	0.3	0.3	0.3	0.8	1.1	1.1	1.1	1.1	1.1	1.1	1.1	:-	
		8	0	0	7		4												721 :										102 :				Ν	
																																22		
AAB31581	ABB69659	ABB59820	AAG06526	AAG06527		ABG11357		AAY22655	AAY23330	ABG21248	AAY97665	<b>л</b> вв63003	1BP28729	AAY75097					AAY38755	ABB59306	AAW78756	AB47131	AAY38757	AAB33115	ABB44563	AAU75883				AAM16187	AAM68370	600	B206	ABB29997
Amino acid sequenc	phila		Arabidopsis thalia		dopsis	l human	human	Human tumour suppr	Human tumour suppr	Novel human diagno	Arabidopsis At-RSH	Drosophila melanog	Streptococcus poly	Neisseria meningit	Neisseria gonorrhe	N. gonorrhoeae ant	Neisseria gonorrho	N. gonorrhoeae ant	Neisseria gonorrho	Drosophila melanog	Human EYA3. Homo	CDIFF-10, Incyte I	Neisseria meningit				ptide	#2599	#2714	Peptide #2621 enco	Human bone marrow	rain ex	n #2602 enc	Peptide #2648 enco

## ALIGNMENTS

01-MAY-2002 (first entry)

PS118 prostate marker immunogenic polypeptide.

AAM50811;

AAM50811 standard; Protein;

35

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(BILL/)
(COHE/)
(COPL/)
(FRIE/)
(GORD/)
                                                                                                                                                                                                                                                                                                                                 PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                   23-APR-1998;
                                                                                                                                                                                                                                    27-DEC-2001.
                                                                                                                                                                                                                                                                     US2001055758-A1
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                (GRAN/
                                                                                                                                                                  23-APR-1997;
   (KRAT/
                                  (HODG/
                   KLAS/
                                                               ) COHEN M.
) COPLPITTS T L.
) FRIEDMAN P N.
) GORDON J.
GRANADOS E N.
) HODGES S C.
) KLASS M R.
) KRATOCHVIL J D.
                                                                                                                                   BILLING-MEDEL P A.
                                                                                                                                                                  97US-0842385
                                                                                                                                                                                                   98US-0065383
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RESULT 2
AAW85472
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    PPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC in non-prostate tissue. PSI18 polypeptides, polynucleotides, CC antibodies, agonists and inhibitors are useful for detecting, CC diagnosing, staying, monitoring, prognosticating, preventing and CC treating (including by genetic immunisation), or determining the CC predisposition of an individual to, diseases and conditions of the CC prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and CC metastases. The PSI18 polypeptides can be produced by expression CC immunogenic peptides are useful for raising PSI18-specific antibodies of diagnostic use. The methods and reagents of the CC invention may palso provide new markers which can differentiate between the clinically important and unimportant prostate cancers C without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising amino acids 283-317 of human prostate-specific PS118 polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynuclearidan antibodies, agonista and intibodies, agonista and intibodies, agonista and intibodies, agonista and intibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Granados EN,
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROBE/) ROBERTS-RAPP L.
                 Billing-Medel PA,
Gordon J, Granado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                23-APR-1998;
                                                                                                                                                                       WO9848054-A1
                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                             EST clone; PS118;
                                                                                                                                                                                                                                                       PS118 protein encoded by consensus sequence.
                                                                                                                                                                                                                                                                                                              AAW85472;
                                                                                                                                                                                                                                                                                                                                        AAW85472 standard;
    Robert-Srapp
                                                         (ABBO ) ABBOTT
                                                                                      23-APR-1997;
                                                                                                                                            29-OCT-1998
                                                                                                                                                                                                                                                                                    25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                              _
                                                                                                                                                                                                                                                                                                                                                                                                                           1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ა
ა
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                 Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>3</u>5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stroupe SD;
    ŗ
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hodges
                                                           LAB.
                                                                                        97US-0842385
                                                                                                                  98WO-US08239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen
dges SC,
     Russell
                                                                                                                                                                                                                           prostate
                            Cohen M,
                                                                                                                                                                                                                                                                                                                                         Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
Hodges SC, Klass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M, Cop
                                                                                                                                                                                                                           tumour tissue; prostatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coplpitts TL, Friedman ass MR, Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 180; DB 2
Pred. No. 1e-18;
                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                  Klass
                 Friedman PN;
MR, Kratoch
                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                        35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                 Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN, Gordon J;
Roberts-Rapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 3
AAM50809
ID AAM5
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δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a cDNA library made from prostate tumout tissue: Recombinant PS118 protein is used to detect PS118 -specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutlos, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 199
N-PSDB;
                  Billing-Medel PA,
Granados EN, Hode
Russell JC, Stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17;
WPI; 2002-187683/24
                                                                                                                                                        (BILL/)
                                                                                                                                                                                                                                                                                                          prostatitis;
                                                                                                                                                                                                                                                                                                                   PS118; prostate; marker; prostate cancer; tumour; benign prostatic hyperplasia; prostatic intraepit
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                   AAM50809;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAM50809 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           risk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of
                                                                                                                                                                                                                 23-APR-1998;
                                                                                                                                                                                                                                       27-DEC-2001.
                                                                                                                                                                                                                                                             US2001055758-A1
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       PS118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New P118 nucleic acid and proteins - used for diagnosis
                                                                                                                                               (COPL/)
                                                                                                                                                                                           23-APR-1997;
                                                                 (ROBE/)
                                                                                         KLAS,
                                                                                                              (GRAN/)
                                                                                                                         (GORD/)
                                                                                                                                   (FRIE/)
                                                                              KRAT,
                                                                                                    HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-610000/51:
DB; AAV82812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                      prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100 35; Conservative
               JC,
                                                                                                                                                        BILLING-MEDEL P
COHEN M.
                                                                                                  GRANADOS E N. HODGES S C.
                                                                                                                         GORDON J.
                                                                                                                                  COPLPITTS T L. FRIEDMAN P N.
                                                                           KLASS M R.
KRATOCHVIL J
                                                                 ROBERTS-RAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 93-94; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518
                    Hodges SC,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostatic
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                           97US-0842385
                                                                                                                                                                                                                                                                                                                                                    marker partial sequence
                                                                                                                                                                                                                 98US-0065383
                                                                                                                                                                                                                                                                                                         diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                  r D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, especially cancer,
                               M, Coplpitts TL,
Klass MR, Kratoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                         518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 180; DB 19;
Pred. No. 2.4e-17;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         A
                               ts TL, Friedman Kratochvil JD,
                                                                                                                                                                                                                                                                                                                    intraepithelial neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
                                                                                                                                                                                                                                                                                                                                 metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                            PN,
                               PN, Gordon J;
Roberts-Rapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 4
ABG09728
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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DB; AAS73915.
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2000US-0649167.
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Pred. No. 2.4e-17;
Mismatches 0;
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RESULT 5
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Matches 35
                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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DB; AAS73918.
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35; Conserv
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2000US-0649167
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100.0%; Pred. No. 1e-16;
0. Mismatches 0;
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    is useful as hybridisation probes,

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Claim

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No 40090;

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RESULT 6
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
The
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polymerase chain reaction (PCR) primers, oligomers, and for c
and gene mapping, and in recombinant production of (II). The
                                                                        New isolated nucleic genes from Drosophila
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11-JUL-2000; 2000US-0614150
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interactions -
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invention
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isolated
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Pred. No. 1.1
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nucleic
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RESULT 7
ABG06957
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Best Local Similarity
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL018176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess blodypersity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 37316; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG06957 standard; Protein; 253 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                food supplement; medical
                                                                                                                                                                                                                                                                                                                                                                                                 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 SKSSRPSSAGVVIDETQSEEEESQSSE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping;
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51.9%;
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imaging; diagnostic; genetic
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RESULT 8
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB60540 standard;
                                                            The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                     Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                       New isolated nucleic acid
genes from Drosophila and
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                                      Sequence
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15; Conserv
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                                      1403
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2000US-0614150
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32.8%;
38.1%;
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Pred. No. 2
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Pred.
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                                                                          format directly from
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            Length 1403;
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Best Local Similarity

Query Match Best Local Similarity

32.2%;

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RESULT 9
AAU42806
ID AAU4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                         and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                 nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-616774/71.
N-PSDB; AAS59518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome;
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                                                                                                                                                                                                                                                the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and ostcomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
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Sequence
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                                                                                                                                                                                                                                                                                                                                                            Example
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endophthalmitis; k
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2000US-208841P.
2000US-216747P.
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S, Carter D;
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                                                                                                                                                                                                                                                                                                               immunogenic
are used in
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RESULT 10 ABB70235

ABB70235;

26-MAR-2002

WO200171042-A2

pharmaceutical. Drosophila;

27-SEP-2001

ABB70235 standard;

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Matches

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences (ABL01840
(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
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2000US-0614150.
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                                                              Peptide; 102
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                                                                                                                                                                                                                                                                                Score 57; DB 22; Pred. No. 7.5;
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                                                                                                                                                                                                                                                                                                       Length 345;
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signalling and
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                                                                                                      RESULT 12
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Matches 12
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trom human breast and BT 4/4 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less blas
                                                                                                                                                                                                                                                                                                                                                                                                     probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid puseful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Sequence
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    23-JAN-2002
                                              ABB20603;
                                                                                     ABB20603 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probes for measuring gene expression in a sample derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-496933/54.
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                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                   l Similarity
12; Conserv
                                                                                                                                                                                                                                        3 QSESSTPSTGGFSGKETPSEDDRSQSREHM 32
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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(first entry)
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                                                                                         Protein; 102
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                                                                                                                                                                                                                                                                                   Score 56; DB Pred. No. 2.5; 6; Mismatches
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ABL14338

23-MAR-2000; 11-JUL-2000;

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RESULT 11 ABB29997

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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, by measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from the .wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15;
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04-OCT-2000;
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  Homo sapiens
                                               epilepsy;
                                                               Human; brain expressed exon; gene expression analysis; microarray; Alzheimer's disease; multiple sclerosis; so
                                                                                                                                  Human brain
                                                                                                                                                                             05-NOV-2001
                                                                                                                                                                                                                        AAM56001;
                                                                                                                                                                                                                                                               AAM56001 standard;
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12; Conservative
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2000US-0207456.
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                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                           entry)
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Pred. No. 2.5;
6; Mismatches
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                                                                                                                                  exon
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                                                                                                                                  encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vascular system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                  protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directly from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                  28106
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AAM68370
    YEAR ON WAY OF THE PER STREET 
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Best Local S
Matches 12
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one o
                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic brains -
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                               WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                microarray;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM68370 standard; Protein; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention provides a number of single exon nucleic bes which are derived from genomic sequences expressed in the sequences {\bf e}_{\rm c}
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                                                                                                                                                                                                                                                                                                                                                                                                                    marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                                                                                                                                                                                                                                                  cancer;
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                      marrow
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2000US-0632366
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                exon; gene expression ; lymphoma; myeloma.
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DB 2.5;

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Length 102

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RESULT 15
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Matches 12
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encode by one such probe. The SENPs are derived from human HeLa cells. The SEN
                                                     Claim 27; SEQ ID No 21013; 487pp; English.
                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                WPI; 2001-488901/53.
                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                        WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2621 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM16187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 28676; 658pp + Sequence Listing; English
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                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNESQSPQ----EPEEGPSEDDKAEGEEEM 52
                                                                                                                                                           Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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Pred. No. 2.5;
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 sequence is a peptide encoded rom human HeLa cells. The SENPs
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Query Match
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Search completed: June 17, Job time: 12,0952 secs
                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                        can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                cervical cancer
                                                               27 QNESQSPQ----EPEEGPSEDDKAEGEEEM 52
                                                                                  QSESSTPSTGGFSGKETPSEDDRSQSREHM 32
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                 2003, 11:55:58
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Pred. No. 2
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180
1 SFQSESSTPSTGGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
4: /cgn2_6/ptodata/1.
5: /cgn2_6/ptodata/1.
6: /cgn2_6/ptodata/1.
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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US-09-065-383-27
US-08-910-925-1
US-08-465-167A-24
US-08-68-45-528C-10
US-08-627-820-24
US-08-627-820-24
US-09-051-982A-5
US-09-051-982A-5
US-09-051-982A-1
US-08-893-852A-1
US-08-893-852A-1
US-09-556-877-195
US-09-620-412C-357
US-09-620-412C-179
US-09-347-8818-2
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US-09-065-383-29
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10 6391543
WATI
  35 amino acids
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ALIGNMENTS

APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: FOR DETECTING DI
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBORT LABORATORIES
STREET: 100 Abbort Park Road
CITY: Abbort Park
STATE: IL INFORMATION FOR SEQ ID NO: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/842
APPLICATION UNMBER: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,44 REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE: SEQUENCE CHARACTERISTICS COUNTRY: USA ZIP: 60064-3500 INFORMATION: Application US/09065383 COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GORDON, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D. BILLING-MEDEL, PATRICIA 08/842,385 35,441 29: 6084.US.P1 AND METHODS USEFUL DISEASES OF THE PROSTATE

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                                            ; MOLECULE TYPE: No. 6391543e US-09-065-383-27
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Best Local Similarity 100
Matches 35; Conservative
 Best Local Similarity
               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                             INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
                                                                                                                                                         REFERENCE/DOCKET NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6084.US.P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPAX: 847/938-2623
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/84
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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SOFTWARE: FastSEC
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                                                                        TOPOLOGY:
                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                    NAME: Becker, Cheryl REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Abbott Laboratories
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: DOS
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RUSSELL, JOHN C
STROUPE, STEPHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRATOCHVIL, JON D. ROBERTS-RAPP, LISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRANADOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BILLING-MEDEL, PATRICIA
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                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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S, STEVEN C.
, MICHAEL R.
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100.0%;
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REAGENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33
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Pred. No. 1e-18;
 Score 180; DB 4;
Pred. No. 2.6e-17;
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            Length 518;
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RESULT 4
US-08-465-167A-24
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US-08-910-925-1
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                                                                                 Sequence 24,
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                                                                    Patent No.
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Best Local Similarity
                                          GENERAL INFORMATION: APPLICANT: Fikes,
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APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: FIBRNOT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                APPLICANT:
APPLICANT:
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    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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                                                                                   Application US/08465167A
                                                                                                                                                                                                                                                                                                                                                                717 amino acids
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Shah, Purvi
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Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
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                                           Fikes, John D.
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41.2%;
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
               COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DA
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-AUG-1993 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                              PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 42.4 nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/103,623 FILING DATE: 06-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                COUNTRY:
                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 QGASAFPTTINFTRQRQPSEG--SSSREEEGPS 89
                                                                                                                                            ESSEE: Felfe & Lynch
ET: 805 Third Avenue
: New York City
E: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
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                                                                                                                10022
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linear
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                                                                                                                                                                                                                                                              REJECTION ANTIGEN
                                                                                                                                                                                                                                                                                                            Charles;
                                                                                                                                                                                                                                                                            ISOLATED NUCLEIC ACID MOLECULE
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US/08/993,118
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Pred. No.
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22;
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US-08-845-528C-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08845528C Patent No. 6027924
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Best Local S
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                 TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: APril 25, 1
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schoftel
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                               STREET: 800 ....
CITY: New York City
STATE: New York
                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                          APPLICATION NUMBER: US/08/8
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                         NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: 1
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             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                              TELEPHONE:
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                                                LENGTH:
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14; Conservative
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DE SMET,
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linear
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                                                                                                              (212) 688-9200
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             single stranded
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42.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charles;
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                                                                                                                                                                                                                                                                                                                              3.5 inch, 360 kb storage
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Pred. No.
                                                                                                                                                LUD 5455
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27.8%;

Score 50;

DB 3;

Length 309

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Patent No. 6464980
GENERAL INFORMATION:
                                                                     Sequence 5, Application US/08549004A Patent No. 5969101
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                        GENERAL .INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                 APPLICANT: PENDERGAST, APPLICANT: DAI, ZONGHAN
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/103,623
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                        59
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14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 309 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                    PENDERGAST, ANN MARIE
                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                               27.8%;
                                                                                                                                                                                                                                                                                                                                                                                            linear
ABL-INTERACTOR PROTEIN
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                                                                                                                                                                                                                                                                               Score 50; DB
Pred. No. 22;
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US-09-051-982A-5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                   ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.
              APPLICATION NUMBER: U5/09/051,982A FILING DATE: 08-UUL-1998 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J. REGISTRATION UMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-193
                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                  STREET: 1100 NOI CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: Patentl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 SVNQRNRTYSSSGSSGPSHPS--SRSSSRENSG 212
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                                                                                                                                                                                                                                                                                                                     1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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linear
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                                                                                                                ; TYPE: PRT; ORGANISM: Homo sapien US-09-332-295-2
                                                                                                                                                                                                                                                                                                                                                           US-09-332-295-2
                                                                                                                                                                             SOPTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                  Matches
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                          Patent No. 630337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                            APPLICANT: Kaufmann, Joerg
TITLE OF INVENTION: CIF130 INHIBITS CELL CYCLE PROGRESSION
FILE REFERENCE: 200130.456 / 1513.003
CURRENT APPLICATION NUMBER: US/09/332,295
CURRENT FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-208-742-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/208,742 CURRENT FILING DATE: 1998-12-10
                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 1453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: CIF150/hTAFII150 is Necessary for Cell ITLE OF INVENTION: Cycle Progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Kaufmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 1261
                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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les 14; Conservative
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SSTPSTGGFSGKETPSEDDRSQSREHMGES 35
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                                                  Conservative
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36.7%;
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                                                  Score 50; DB 4;
Pred. No. 1.2e+02;
5; Mismatches 14
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Pred. No.
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Pred. No.
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                                                                                 Length 1261;
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US-09-709-979-2
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US-09-709-979-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 09/332,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/709,979
CURRENT FILING DATE: 2000-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 200130.456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kaufmann, Joerg
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SEQUENCE CHARACTERISTICS:
                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                              APPLICATION NUMBER: US/08/893,852A FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                   TELEPHONE:
                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                                                                                                                                                              CATION NUMBER:
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                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                                                                                             Diskette
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36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEW HUMAN GROWTH REGULATOR PROTEIN
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                                                                                    PF-0341 US
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Pred. No. 1.2e+02;
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; IMMEDIATE SOURCE:
; LIBRARY: TMLR3D'
; CLONE: 508302
US-08-893-852A-1
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US-08-910-925-4
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Best Local Similarity 37.9
Matches 11; Conservative
                                                       Matches
                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1684843
                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/910,925
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: HUMAN PININ SPLICE VARIANT JMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 POR CITY: Palo Alto
                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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615 SSRTSSSSSTTSGSSSRDSSSSTTSSSESRSRSR 648
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                                                                                                                                                                                                  amino acid
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3174 Porter Drive
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                                                       Conservative
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                                                                                                                                                                    linear
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37.9%;
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Pred. No. 65;
                                                                     Score 49.5;
Pred. No. 68;
                                                       Mismatches
                                                                                  DB 4;
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                                                                                   Length 703;
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RESULT 15

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CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 357
LENGTH: 683
TYPE: PAT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-357
Search completed: June 17, 2003, 12:03:39 Job time: 4.2284 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 357, Application US/09620412C Patent No. 6448234;
                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Steven P. Fling
                                                                                                                                                         Local Similarity 34.3 ses 12; Conservative
                                                                             173 SSKSGSSTPQDGGAASSGAPSGDQSISANACLAKS 207
                                                                                                                   1 SFQSESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                              27.2%;
                                                                                                                                                         Score 49; DB of Pred. No. 78; 5; Mismatches
                                                                                                                                                              5.
                                                                                                                                                                                                 DB 4; Length 683;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       Published_Applications_Aa:*

1: /cgn2_6/ptodata/1/pubpaa/us

2: /cgn2_6/ptodata/1/pubpaa/us

3: /cgn2_6/ptodata/1/pubpaa/us

4: /cgn2_6/ptodata/1/pubpaa/us

5: /cgn2_6/ptodata/1/pubpaa/us

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6: /cgn2_6/ptodata/1/pubpaa/us

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13: /cgn2_6/ptodata/1/pubpaa/us

14: /cgn2_6/ptodata/1/pubpaa/us

15: /cgn2_6/ptodata/1/pubpaa/us

16: /cgn2_6/ptodata/1/pubpaa/us

17: /cgn2_6/ptodata/1/pubpaa/us

18: /cgn2_6/ptodata/1/pubpaa/us

19: /cgn2_6/ptodata/1/pubpaa/us

10: /cgn2_6/ptodata/1/pubpaa/us

11: /cgn2_6/ptodata/1/pubpaa/us

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Gapop 10.0 , Gapext 0.5
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180
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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413	309	275	253	212	758	105	105	68	80	79	77	65	65	42	91	737	102	Query Match Length	
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US-10-085-108-10	US-09-766-889A-2	US-09-755-456-9	US-09-864-761-37733	US-09-764-891-4686	US-09-904-987-5	US-09-955-807-14	US-09-955-807-2	US-09-955-807-15	US-09-955-807-16	US-09-955-807-3	US-09-955-807-4	US-09-955-807-10	US-09-955-807-5	US-09-955-807-9	US-10-090-035-16	US-10-228-931-4	US-09-864-761-35901	ID	
Sequence 10, Appl	Sequence 2, Appli	Sequence 9, Appli	Sequence 37733, A	Sequence 4686, Ap	Sequence 5, Appl	Sequence 14, App	Sequence 2, Appl	Sequence 15, Appl	Sequence 16, App	Sequence 3, Appl	4	Sequence 10, Appl		Sequence 9, Appl	· Sequence 16, Appl	Sequence 4, Appli	Sequence 35901,	Description	

## ALIGNMENTS

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R APPLICATION UMBER: PCT/US01/00661 R FILING DATE: 2001-01-30	APPLICATION N	FILING DATE	FILING DATE	APPLICATION N	FILING DATE	APPLICATION N	FILING DATE	R APPLICATION NUMBER: PCT/US01/00669	APPLICATION I	FILING DATE	R APPLICATION NUMBER: PCT/US01/00667	R FILING DATE: 2001-01-30	APPLICATION N	FILING DATE: 2000-09-27	APPLICATION I	FILING DATE	APPLICATION N	FILING DATE: 2000-08-03	APPLICATION	FILING DATE		FILING DATE: 2000-02-04		ENT ETITIO DATE: 2001-05-23	-	OF INVENTION:	OF INV		Hanzel, Dav	Rank, David F	APPLICANT: Penn, Sharron G.	8763A1	Sequence 35901, Application US/09864761	US-09-864-761-35901	
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RESULT 2
US-10-228-931-4
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RESULT 3
US-10-090-035-16
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 737
TYPE: PRT
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                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10228931 Publication No. US20030051258A1
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                                                                                                                                                    Matches
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CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US/09/772,647
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron P
TITLE OF INVENTION: Animal Model System for
FILE REFERENCE: 960296.97613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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                                                                                327 AESPQPASG----NSPSEDDRSKS 346
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12; Conserv
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EXPRESSED IN BT474, SIGNAL = 1.1

EXPRESSED IN BONE MARROW, SIGNAL
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IN HEART, SIGNAL = 0.98
IN HELA, SIGNAL = 2.1
IN HBL100, SIGNAL = 1.9
IN BRAIN, SIGNAL = 1.2
HIT: BE792924.1, EVALUE 1.40e-01
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IN ADULT LIVER, SIGNAL = 1.4
                                                                                                                                                                  Score 53.5;
Pred. No. 60;
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Pred. No. 3;
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                                                                                                                                                  Mismatches
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; LENGTH: 91
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-090-035-16
                                                                                                                                                        RESULT 5
US-09-955-807-5
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 16
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 12
                                                                                  GENERAL INFORMATION: APPLICANT: Lok, Si
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Patent No. Ubzu-
Patent No. Ubzu-
Patent INFORMATION:
                                                                                                                    Sequence 5, Application US/09955807 Patent No. US20020132996A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
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Best Local Similarity
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                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secretory Protein-48 FILE REFERENCE: 98-17C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
FILE REFERENCE: 98-17C1
                   TITLE OF INVENTION:
                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4:
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                              9 PSTGGFSG----KETPSEDDRSQ 27
                                                                                                                                                                                                                                                                                                              Similarity
                                Sheppard, Paul O.
Kindsvogel, Wayne
Bort, Susan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bort,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kindsvogel, Wayne
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                Secretory Protein-48
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Pred. No. 7.6;
1; Mismatches
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Pred. No. 5;
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US-09-955-807-10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-807-5
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US-09-955-807-4
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FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Lok, Si
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Best Local Similarity
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LENGTH: 65
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                CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-09-19
                                                                                    APPLICANT: Kindsvogel, Wayne
APPLICANT: Bort, Susan J.
TITLE OF INVENTION: Secretory
FILE REFERENCE: 98-17C1
                                                                                                                                                        APPLICANT:
APPLICATION NUMBER: 09/410,603
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12; Conserv
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Bort, Susan J.
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52.2%;
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Pred. No. 8.
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8.2;
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; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-807-4
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                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Kindsvogel, Wayne
APPLICANT: Bort, Susan J.
TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-10-01
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Best Local S
Matches 12
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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Best Local :
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 16 LENGTH: 80
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                                                PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
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APPLICANT: Sheppa
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APPLICANT: Sheppa
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12; Conserv
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Pred. No. 10;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-955-807-16
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; ORGANISM: Homo sapiens
US-09-955-807-15
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US-09-955-807-15
                                             ; ORGANISM: Homo sapiens US-09-955-807-2
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                                                               SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 105
TYPE: PRT
ORGANITOR:
Query Match
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15
LENGTH: 89
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Best Local :
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Best Local Similarity 52.2%;
Matches 12; Conservative
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TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-99-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-10-01
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
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TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lok, Si
APPLICANT: Sheppar
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Bort, Susan J.
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            28.3%;
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Pred. No.
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Pred. No. 12;
              Score 51;
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              DВ
              10;
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              Length 105
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TITLE OF INVENTION: Secretory Protein-48
FILE REFERENCE: 98-17C1
CURRENT APPLICATION NUMBER: US/09/955,807
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/102,679
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 09/410,603
PRIOR FILING DATE: 1999-10-01
VINDER: OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-807-14
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US-09-955-807-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09904987 Patent No. US20020037908A1 GENERAL INFORMATION:
                                                                                              Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09955807 Patent No. US20020132996A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 12; Conser
                                                                                                                Query Match
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Best Local S
                                                                                                                                                                    ORGANISM: homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / NM_016835
DATABASE ENTRY DATE: 2001-02-13
RELEVANT RESIDUES: (1)..(758)
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/904,987
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: No. US20020037908A1actyl, Inc.
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prep
TITLE OF INVENTION: Protein Assembly or Aggregation
FILE REFERENCE: 42108/26146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lok, Si
APPLICANT: Sheppard, Paul O.
APPLICANT: Kindsvogel, Wayne
APPLICANT: Bort, Susan J.
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version'3.0
                                                                                                                                                                                                                                                                    LENGTH: 758
TYPE: PRT
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282 SEPDGPSVGRAKGQDAPLEFTFHVEITPNVQKEQAHSEEHLGRA 325
                                                                      28.3%;
l Similarity 27.3%;
l2; Conservation
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12; Conser
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                                      4 SESSTPSTGGFSGKETPSE------DDRSQSREHMGES 35
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                                                                          Score 51; DB Pred. No. 1.3e 7; Mismatches
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Pred. No. 14;
3; Mismatches 4; Indels
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                                                                                            1.3e+02;
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: OTHER INFORMATION: Xaa equals any of the national information in th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
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atent No. US20020048763A1
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CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-02-04
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TYPE: PRT
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                                                                         APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04 APPLICATION NUMBER: US 60/236,359 APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
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Chen, Wensheng
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FILING DATE: 2001-01-29
203 SDEQTPSRDDDSQSR 217
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                 15 SGKETPSEDDRSQSR 29
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Pred. No. 52;
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IN BT474, SIGNAL = 1.4
IN FETAL LIVER, SIGNAL = 1.7
IN BONE MARROW, SIGNAL = 1.4
IN LUNG, SIGNAL = 4.6
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AI350947.1, EVALUE 1.00e-78
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                            GenCore version 5.1.6 (c) 1993 - 2003 Compus
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                            AF3242
S22997
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F72645
T34000
                                                                                      JN0785
D88450
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F81045
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traK protein - Esc
transfer origin pr
hypothetical prote
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hypothetical prote
protein kinase C (
protein kinase C (
                                                                          Carbon catabolite protein F21H11.2 ( short neurotoxin 1
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hypothetical prote
zinc-finger protei
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collagen alpha 2(I
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Best Local
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Result

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Minimum DB Maximum DB

Searched

Sequence:

Database

vitellogenin I pre	T29088	N	1912	27.8	50	45
hypothetical prote	A71517	N	1770	27.8	50	44
natural killer cel	A47328	ப	1403	27.8	50	43
SERA antigen/papai	D71617	2	930	27.8	50	42
hypothetical prote	T29372	2	829	27.8	50	41
	T08745	N	819	27.8	50	40
hypothetical prote	T45059	N	735	27.8	50	39
hypothetical serin	T41586	N	710	27.8	50	38
chemotaxis protein	S70180	ພ	686	27.8	50	37
chemotaxis sensor	D72346	N	671	27.8	50	36
hypothetical prote	т29917	N	454	27.8	50	35
melanoma antigen M	JC2358	N	280	27.8	50	34
hypothetical prote	A84227	N	579	28.1	50.5	ω ω
nucleoporin p62 -	S41819	N	522	28.1	50.5	32
hypothetical prote	T18651	N	430	28.1	50.5	31
cnjB protein - Tet	S42136	N	1748	28.3	51	30

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arailes, W.; Buysshaert, C.; Dasseville, R.; De Clerck, Lemcke, K.; Mayer, K.F.X.

A;Reference number: Z24487
A;Accession: T48187
A;Accession: T48187
A;Molecule type: DNA
A;Residnes
                                                                                                                                                                                                                                                                                                       hypothetical protein F7A7.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48187
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Cle ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X:
submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Girdham, C.H.; Glover, D.M. Genes Dev. 5, 1786-1799, 1991
Genes Dev. 5, 1786-1799, 1991
A;Title: Chromosome tangling and breakage at anaphase result from mutations in lodest A;Reference number: A40580; MUID:92009170; PMID:1916263
A;Accession: A40580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lodestar maternal-effect protein - fruit fly (Drosophila melanogaster)
%;Alternate names: probable nucleoside triphosphate binding protein lodestar
C;Species: Drosophila melanogaster
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000
C;Accession: A40580; S19008
                                                                                  A; Map position: 5
A; Introns: 65/3; 263/3;
A; Note: F7A7.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:X62629; NID:g8187; PIDN:CAA44496.1; PID:g8188
C;Genetics:
A;Gene: lodestar
                                                                                                                                              A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-621 <BEV>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-974 <GIR>
Query Match
Best Local S
Matches 12
    12;
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14; Conserv
                     Similarity
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31.1%;
ilarity 38.7%;
Conservative
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                                                                                                     289/3; 403/1; 469/3; 495/2; 529/2; 592/3
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Score 56; DB:
Pred. No. 20;
6; Mismatches
    6;
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7.1;
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    13;
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Read, T.D.; Peterson, S.; Hei on, J.B.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Accession: B95010
A; Accession: B95010
A; Rocession: B95010
    C; Species: Neisseria
C; Date: 31-Mar-2000 #
C; Teccession: F81045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein spr0080 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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A; Residues: 1-89 < KUR>
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A; Residues: 1-89 <KUR>
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                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                           hemagglutinin/hemolysin-related protein NMB1768 [imported] -
                                                                                    F81045
                                                                                                                                                                                                                                                                                                                                              Genetics:
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10; Conserv
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                                                                                                                                                                  ESQSATKDGGQTAGKETAGEDESANQTQEISQ 86
                                                                                                                                                                                                       QSESSTPSTGGFSGKETPSEDDRSQSREHMGE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESQSATKDGGQTAGKETAGEDESANQTQEISQ 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVEHKSSIYAVGGYDGKEYLNTAERFDPREH 505
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                                                                                                                                                                                                                                                                                                                                                                GB:AE007317;
                      #sequence_revision
                                         meningitidis
                                                                                                                                                                                                                                                                30.6%;
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                                                                                                                                                                                                                                                                                                                                                              PIDN: AAK98884.1; PID: g15457615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arnold, J.; Blaszczak, L.; Burgett, Lefkowitz, E.J.; Lu, J.; Matsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                              Score 55;
Pred. No.
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                      31-Mar-2000 #text_change
                                                                                                                                                                                                                                                              3.8;
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                                                                 Neisseria meningitidis
                          19-Jan-2001
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                                                                 (sti
protein kinase C (EC 2.7.1.-) epsilon - rat C;Species: Rattus norvegicus (Norway rat) C;Cate: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999 C;Accession: B28163; B26408; S00216 R;Ono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y. Biol. Chem. 263, 6927-6932, 1988 J. Biol. Chem. 263, 6927-6932, 1988 A;Title: The structure, expression, and properties of additional members of A;Reference number: A92717; MUID:88198270; PMID:2834397 A;Accession: B28163 A;Molecule type: DNA A;Residues: 1-737 <0NO>
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of composed 1 of the plant Arabidopsis A; Reference number: A86141; MUID:21016719; pMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F15I1.23 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
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D96582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
                                          γ
                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-715 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: D96582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-2514 <TET>
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                                                                                                                                                                        A; Map position:
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                                                                                     Matches
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Best Local
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14; Conserv
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16; Conser
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QSQSETYHQTQKSGLMSAGIGFTIGSKTNTQENQSQSNEHTGST 1580
SASSSTSSPTIGGLSLLFSGASVKSSSSSSSSHPSVGE 77
                                    SFQSESSTPSTGG----FSGKETPSEDDRSQSREHMGE 34
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                                                                                                         Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.5;
Pred. No. 1.
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Conway, A.B.; Conway, A.R.; Creasy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                     Mismatches
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                                                                                                       DB
42;
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                                                                                       16;
                                                                                                                              Length 715;
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                                                                                                                                                                                                                                                                                                                                                                                          Southwick, A.M.; Sun, Davis, R.W.
                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.; White, reasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khaykin, E
Maiti, R.;
                                                                                     Gaps
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Dougherty, B
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strain MC58.
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Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A;Title: Isolation of cDNA clones encoding protein kinase A;Reference number: A94145; MUID:87147193; PMID:3469647 A;Acad. B26408
                                                                                                                                                                                                                                                                                                                                                            F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:403-292/Domain: protein kinase c zinc-binding motif
F:406-668/Domain: protein kinase homology <KIN>
F:406-668/Domain: protein kinase homology <KIN>
F:4170-201, 207/Dainding site: zinc (His, Cys, Cys, Cys) #status predicted
F:170-201, 207/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:437,456,532,534/Anctive site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-737 <SCH>
C; Function:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning; Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl C; Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; plockeywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid by the content of the con
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F:243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:406-668/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:414-422/Region: protein kinase ATP-binding motif
F:170,201,204,220/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted F:183,186,209,12/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F:243,273,276,292/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted F:437,456,532,534/Active site: Lys Glu, Asp, Lys #status Predicted F:437,456,532,534/Active site: Lys Glu, Asp, Lys #status Predicted F:437,456,532,534/Active site: Lys Glu, Asp, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Unique substrate specificity and A;Reference number: S02270; MUID:89137541; A;Accession: S02270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Schaap, D.; Parker, P.J.; B; FEBS Lett. 243, 351-357, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase C (EC 2.7.1.-) epsilon - mouse C:Species: Mus musculus (house mouse) C:Date: 30-Sep-1992 #sequence_revision 30-Sep C:Accession: S02270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni A; Note: activity is calcium-independent, phospholipid-dependent, and activated by diacy C; Superfamily: protein kinase C adelta; protein kinase C alon-binding repeat homology; p C; Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester
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A;Molecule type: mRNA
A;Residues: 397-447,'GQRGLHDDREEDFGSGAET',467,'LSNPTLLLLPDQGPPLLRQ',487-545,'C',547-636
A;Cross-references: GB:M15523; NID:g206192; PIDN:AAA41877.1; PID:g206193
C;Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene a
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F;170-220/Domain:
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Best Local S
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12; Conser
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48.0%;
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                                                                                            Score 53.5; D
Pred. No. 50;
5; Mismatches
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Pred. No. 50;
5; Mismatches
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C; Genetics:
A; Gene: AblBP3
C; Superfamily: SH3 F; 335-382/Domain: SH
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G01936
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                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-390 <REN>
A; Cross-references: EMB
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A; Accession: G01936
A; Status: prelimina
                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: G08875
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C; Date: 21-Dec-1996 #sec
C; Accession: G01936
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A; Residues: 1-384 <WIL>
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142
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                                                    l Similarity
15; Conser
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SVNQRNRTYSTSGSSGGSHPS--SRSSSRENSG
                        SFQSESSTPSTGGFSGKETPSEDDRSQSREHMG
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                                                     Conservative
                                                                                                           SH3
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SH3 homology <SH3>
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ce: clone K11
                                                                                                                                                              EMBL: U31089;
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                                                                                                                                                                                                        translated
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(man)
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                                                                 29.4%;
45.5%;
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                                                    2;
                                                                                                                                                              NID:g987264;
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Pred. No.
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Pred.
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30;
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30;
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RESULT T26702

11

hypothetical

protein

Y38H6C

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Caenorhabditis

elegans

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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.Fültle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                               hypothetical protein F14010.5 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: C86337 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
                                                                                                                                                                                                                                                                                   RESULT
C86337
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R;Dleck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, J. Cell Biol. 142, 499-509, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
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A; Introns: 25/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat A;Reference number: Z22249; MUID:98345363; PMID:9679147 A;Accession: T42761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bassoon protein
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A; Residues: 1-814 <WIL>
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A; Accession: T26702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Alternate names: brain-specific synap;Species: Rattus norvegicus (Norway ra;Date: 11-Jan-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Description: may be involved in cytomatrix organization at the site of neurotransmitte;Note: component of the presynaptic cytoskeleton ;Reywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; Experimental source: strain Sprague Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Caenorhabditis elegans; Date: 15-Oct-1999 #sequence_revision; Accession: T26702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: mRNA
;Residues: 1-3938 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: CESP:Y38H6C.14
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Best Local
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16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                  SSTPSTGGFSGKETPSEDDRSQSREH 31
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45.7%;
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Pred. No. 64;
4; Mismatches
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Pred. No. 3.1e+02.
4; Mismatches 1:
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                                                                                                                                                             y, A.B.; Conway, A.R.; Creasy, T.H.;
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                                                                                S.; Khaykin, E.; S.; Maiti, R.; Ma
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                                              Η.,
                                                                                                                                                               O.; Alonso; Dewar, K.
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                                                Tallon,
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                                                                                                       A; Molecule type: mRNA
A; Residues: 1-775 < YAM>
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R; Nietfeld, W.;
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                                                                                                                                             A; Status: preliminary
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C; Superfamily: collagen alpha 1(IV) chain
C; Keywords: coiled coil; extracellular mai
                                                                                                                                                              R; Yamaguchi, N.; Sato, N.; Ko, J.S.; Ninomiya, Y. Invest. Ophthalmol. Vis. Sci. 32, 2924-2930, 1991 A; Title: Cloning of alpha1(IV) and alpha2(IV) collagen A; Reference number: A61228; MUID:92010685; PMID:1717398 A; Accession: A61228
                                                                                                                                                                                                                                                                                     collagen alpha 2(IV) chain precursor - rabbit (fragments) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone XlcGF20-1
C; Superfamily: zinc finger protein ZFP-36;
C; Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Blochem. 226, 567-576, 1994
A;Title: Sequence-specific recognition of a repetitive DNA
A;Reference number: S51037; MUID:95094815; PMID:8001572
A;Accession: S51037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 85-448, 'K', 450-613 <NIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Second-order repeats in Xenopus laevis finger proteins A;Reference number: S05632; MUID:90040698; PMID:2509712 A;Accession: S06565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; J. Mol. Biol. 208, 639-659, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Xenopus laevis (African clawed C;Date: 01-Aug-1995 #sequence_revision 01-
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A;Accession: C86337
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Pred. No. 71;
8; Mismatches
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OM protein - protein search, using sw model
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June 17, 2003, 11:48:41; Search time 31.0952 Seconds (without alignments) 690.935 Million cell updates/sec
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Title:
Perfect score:
Sequence: US-09-991-681-27 2698 1 RIRAMAQQVFMLDTO

RIRAMAQQVFMLDTQCSPKT.....VRQAVREWLGRVGRVYDIIV 518

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

45	44	43	42	41	40	39	38	37	36	35	34
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                    PLHSRSSGNNLSSANVKTLEAPV 1729
                                                                                             RPRSGSTGSSL-SVSVRDAEAQI
                                                                                                                               FPKEVKVEKKGEPL------GPRGQDS-PLLQRPQHLMDQGQMRHSFSAGPELLRQDK 432
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R -> W (IN REF. 2).
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and dosage compensation in C. elegans.";
Cell 72:349-364(1993),
-1- FUNCTION: CONTROLS BOTH SEX DETERMINATION AND
COMPENSATION. THESE TWO FUNCTIONS ACT INDEPEND
-1- SUBCELLULAR LOCATION: Nuclear.
-1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYONIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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DOMAIN 443 987
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; FALSE_NEG.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; Metal-binding; DNA-binding;
Developmental protein; Zinc-finger; Metal-binding; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
EYGELDEAGAPSPSEIVVHDEVLQDEVLQPNPKSSKKRGRRRKKTPPHIAKARKVFT---
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Pred. No. 0.
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C2H2-TYPE.
MW; 7430D77AC784EA46 CRC64;
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DOSAGE COMPENSATION DOMAIN 2.
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RESULT 3
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Matches 85
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 54.6 kDa protein F59B10.2 in chromosome
F59B10.2.
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                            LLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKL---
                                                                           PTESSFESSSDSSSTSESSTSSESSSSSASESESESKSESQVSSSKTSTSKASSSKAYGSD
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91335211; PubMed-1651563;
Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horil A.,
Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.,
Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,
Preisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B.;
"Mutations of chromosome 5q2l genes in FAP and colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinzler K.W., Nilbert M.C., Vogelstein B., Bryan T.M., Levy D. Smith K.J., Preisinger A.C., Hamilton S.R., Hedge P., Markham Carlson M., Joslyn G., Groden J., White R., Miki Y., Miyoshi Y Nishisho I., Nakamura Y., "Identification of a gene located at chromosome 5q21 that is min colorectal cancers."; Science 251:1366-1370(1991).
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                              EMBL; M62397; AAA52069.1;
PIR; A33166; A33166.
PIR; A38434; A38434.
Genew; HGNC:6935; MCC.
                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES TYPES.
-1- DISEASE: IS PROBABLY INVOLVED IN EARLY STAGES OF COLORECTAL NEOPLASIA IN BOTH SPORADIC AND FAMILIAL TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 253:665-669(1991).
-I- FUNCTION: CANDIDATE FOR THE PUTATIVE COLORECTAL TUMOR SUPPRESSOR GENE LOCATED AT 5021.
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Mammalia; Eutheria;
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01-NOV-1991
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Primates;
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                         /FTId-VAR_005143.
                                                                        /FTId-VAR_005142.
S -> L (IN COLORECTAL CANCER).
                                                                                                                    /FTId=VAR_005141.
P -> L (IN COLORECTAL
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Best Local S
Matches 92
                        TISSUE=Cervix;
Strausberg R.;
Submitted (DEC-2000) to
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16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                            origin."
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MEDLINE=20296799; PubMed=10835276;
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
SEQUENCE OF
                                                                                                                                       Riva S.,
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                                                                                               Biol.
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Pred. No. 2
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/FTId-VAR_005145.
5D45225FD91CA18F CRC64;
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Flagiello D., Gibaud A., Dutrillaux B., Poupon M.F., Malfoy B.;
"Distinct patterns of all-trans retinoic acid dependent expression
HOXB and HOXC homeogenes in human embryonal and small-cell lung
carcinoma cell lines.";
FEBS Lett. 415:263-267(1997).
-I- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSTITIONAL IDENTIFIES ON THE ANTERIOR-POSTERIOR AXIS.
-I- SUBCELLULAR LOCATION: Nuclear
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HSSP; P02833; 9ANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX FAMILY.
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                                                                         ELLRQDKRPRSGSTGSSLSVSVRDAEAQIQA
                                                                                                                                                                                                                                                                                              SLNPRAEHL-ESPQL---GGKVSFPETPKSDSQTPS----
                                                                                                                                                                                                                                                                                                                                                            SQS--REHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISK
                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt RAKSGPEAALYSHPLPESCLGEHEVPVPSYYRASPSYSALDKTPHCSGANDFEAPFEQRA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPSLALNTYPSYLSQLDSWGDPKAAYRLEQPV--GRPLSSCSYPPSVKEENVCCMYSAEK
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19.3%;
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                                                                                                                                                      PNEIKTEQ--SLAGPKGSPS
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A -> G (IN REF. 3).
MISSING (IN REF. 3).
BD8127FD43C2A37B C
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Pred. No. 0.
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RESULT 6 S3B2\_HUMAN

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                                                                                     Query Match
Best Local
                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEX ASSEMBLY FORMED BY THE SPLICING FACTOR SF3B REQUIRED FOR 'A'
COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF UZ SNRNP TO THE
BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
ESSENTIAL, IT MAY ANCHOR UZ SNRNP TO THE PRE-MRNA. MAY ALSO BE
INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX BELONGS ALSO TO THE
MINOR U12-DEPENDENT SPLICEOSOME, WHICH IS INVOLVED IN THE SPLICING
OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON.

-1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED OF
FOUR SUBUNITS; SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145,
SF3B1/SAP155. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A
12S RAN UNIT TO FORM THE UZ SMALL NUCLEAR REBONUCLEDRROTEINS
COMPLEX (UZ SNRNP). SF3BZ INTERACTS DIRECTLY WITH SF3B4.

-1- SUBCULUAR LOCATION: NUCLEAR (BY SIMILARITY)
-1- SIMILARITY: TO YEAST CUS1. SOME, TO C.ELEGANS ZK632.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 45, Last sequence update)
Splicing factor 3B subunit 2 (Spliceosome associated protein 145) (SAP 145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit).
SF3B2 OR SAP145.
                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE FOLLWARD CO., Reed R.;
Gozani O., Feld R., Reed R.;
"Evidence that sequence-independent binding of highly conserved U2
"Evidence that sequence independent binding of highly conserved U2
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional association of U2 snRNP with the ATP-independent spliceosomal complex E."; Mol. Cell 5:779-787(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                  Spliceosome;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF THE SPLICEOSOME MEDLINE=20337962; PubMed=10882114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=96154048; PubMed=8566756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S3B2_HUMAN
                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                   EMBL; U41371; AAA97461.1;
                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Das R.,
                                                                                     SEQUENCE
                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                           InterPro; IPR003034;
Pfam; PF02037; SAP; 2
                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNP proteins upstream of the branch site spliceosomal complex A. ";
                                                                                                                                                                                                                                                                       605591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. 10:233-243(1996).
                              63;
                                                                                                                                                                                                                              PF02037; SAP; 2.
SM00513; SAP; 1.
                                                                                                                                                                                                                                                                                   HGNC:10769; SF3B2
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                                          Similarity
TNQETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPP---
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106
226
308
676
                             Conservative
                                                                                                                                                                                                            mRNA processing;
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                                          4.0%;
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                             46;
                           Score 108.5;
Pred. No. 3.2;
16; Mismatches
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POLY-PRO
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POLY-PRO
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POLY-GLU
POLY-GLU
POLY-GLU
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                                                                                                                                                                                                               mRNA
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                                                                                   AED669FD0DA5DE31 CRC64;
                                                                                                                                                                                                               splicing;
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                                                       DB
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                             118;
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ABF1_HUMAN
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                                                                              SEQUENCE OF 1151-3703 FROM N.A. KOZIOWICZ A., MCQUETTY Y., Hotic M., KOZIOWICZ A., MCQUETTY Y., Hotic M., Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: Transcriptional activator that binds to the
                                                                                                                                                                                                                "Genome duplications and other features human chromosome 16p and 16q."; Genomics 60:295-308(1999).
                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-1190 FROM N.A. (ISOFORM A).

MEDLINE-99425270; PubMed-10493829;

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Hepatoma;
MEDLINE-92049333; PubMed-1719379;
Morinaga T., Yasuda H., Higashio K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of an ATBF1 neuronal differentiation-dependent manner. J. Biol. Chem. 270:26840-26848(1995).
                                 <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miura Y., T
Tamaoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96070776;
Miura Y., Tam T.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATBF1
                           FUNCTION: Transcriptional activator that sequence of the enhancer element of the a SUBCELLULAR LOCATION: Nuclear.
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  PRODUCTS:
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Ido A., Morinaga
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Pfam; Pr00046; homeobox; 4.
Pfam; Pr00096; zf-C2H2; 20.
ProDom; PD000010; Homeobox; 4.
SMART; SM00389; HOX; 4.
SMART; SM00355; ZnF_C2H2; 21.
SMART; SM00451; ZnF_U1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L32832; AAC14462.1; -.
EMBL; D10250; BAA01095.1; -.
EMBL; AC002044; AAC31674.1; -.
EMBL; AC004943; AAC79153.1; -.
HSSP; P20263; 10CP
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TRANSFAC; T01665; -.
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104155; -.
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027; HOMEDBOX_1; 2.
071; HOMEDBOX_2; 4.
028; ZINC_FINGER_C2H2_1; 14.
157; ZINC_FINGER_C2H2_2; 9.
regulation; Activator; 2inc-finger; Metal-binding;
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Mabuchi N., Yamamura
Matsuda T.;
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CONFLICT
                                                                                                                                                                                          Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasian
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/FTId=VAR_011695.
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Pfam; PF01347; Vitellogenin_N; 1.
SMART; SM00216; VWD; 1.
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InterPro; IPR001747; Lipid_transprt_N.
InterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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SEQUENCE OF 1628-1639,
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
SIGNAL
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                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          k proteins: the 40 kDa yolk plasma glycoprotein is der:
C-terminal cysteine-rich domain of vitellogenin II.";
chim. Biophys. Acta 1244:384-394 (1995).
FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: MAY CONTAIN INTRAMOLECULAR DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: BY Steroids (estrogen).

PTM: PHOSVITIN, AN EGG YOLK STORAGE PROTEIN, IS ONE OF THE MOST HIGHLY PHOSPHORYLATED (10%) PROTEINS IN NATURE.

PTM: CATHEPSIN D IS RESPONSIBLE FOR INTRAOOCYTIC PROCESSING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND THEN SEQUESTERED BY RECEPTOR MEDIATED ENDOCYTOSIS INTO OOCYTES, WHERE IT IS GENERALLY CLEAVED, GIVING RISE TO THE RESPECTIVE YOLK COMPONENTS.
                       1125
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                                                                                                                       Similarity
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                                                                  KRVKKILDDTDNQATRNSRSSSSSSSSISESSESTTSTPSSSSDSDNRAS---
                                                                                     EQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSN
                                            ADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSE------
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POLY-SER.
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SER-RICH.
                                                                                                                                                                                                                                                                                                     LIPOVITELLIN I (BY SIMILARITY).
PHOSVITIN (BY SIMILARITY).
LIPOVITELLIN II (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris P.V., Kaelin C.B., Burtis K.C.;

"Catalytic activity of Pol eta, a new human DNA polymerase related the bacterial DNA polymerase I family and Drosophila Mus308."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: COULD BE INVOLVED IN THE REPAIR OF INTERSTRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99326527; PubMed-10395804; Sharlef F.S., Vojta P.J., Ropp P.A., Copeland "Cloning and chromosomal mapping of the human (POLQ), the eighth human DNA polymerase."; Genomics 59:90-96(1999).
                                                                                                                                                               PRINTS; PR00868; SMART; SM00482; 1
                                                                                                                                                                                                                                                                                                                                             EMBL; AF052573; AAC33565.1; -. EMBL; AF043628; AAD05272.1; -. HSSP; P00582; 1KFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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075417; 09
                                                                                                           Transferase;
                                                                                                                                                                                                                                          InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_polI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY:
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                                                                                     NP_BIND
                                                                                                                                      PROSITE; PS00447;
                                                                                                                                                                                                                                                                                                                          Genew;
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase theta (EC 2.7.7.7) (DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1306
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                                                                                                                                                                                                                 PF00476; DNA_pol_A;
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                                                                                                                                                                                                                                                                                                                       HGNC: 9186;
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1185 1185 L
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                                                                                                                                    DNA_POLYMERASE_A;
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NA polymerase; ATP-binding; D
ATP (POTENTIAL).
L -> F (IN REF. 2).
R -> Q (IN REF. 2).
V -> A (IN REF. 2).
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Best Local S
Matches 101
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pr9937; pr9938;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence u
15-JUN-2002 (Rel. 41, Last annotation
Homeobox protein Meisi (XMeisi).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
Xenopodinae; Xenopus.
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SEQUENCE
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-97202105; PubMed-9049632;

Steelman S., Moskow J.J., Muzynski K., North C., Druck

Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;

"Identification of a conserved family of Meisl-related

genes.";
                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; MEIS1-1 (S
-i- AND MEIS1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE TALE/MEIS HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                  Genome Res. 7:142-156(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
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llarity 21.28;
Conservative
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36, Last sequence up
41, Last annotation
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                 license agreement (See http://www.isb-sib.ch/announce/
license@lsb-sib.ch).
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Mesobatrachia; Pipoidea; Pipidae;
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MW; AECD17A2103F6BDA CRC64;
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frog)
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                                                                                                                                                                                                                                         S; MEIS1-1 (SHOWN SPLICING.
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                                                                                                                                            a collaboration - MBL outstation -
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EMBL; U68387; AAB19197.1; -.
HSSP; P41778; 1DU6.
TRANSFAC; T03390; -.
TRANSFAC; T03391; -.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                   GTA_NPVAC STANDARD; PRT; 5 P4.1447; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence up. 01-NOV-1995 (Rel. 32, Last annotation of the control of the cont
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                 Ayres M.D., Howard
                                        MEDLINE=94303173; PubMed=8030224; Ayres M.D., Howard S.C., Kuzio J.
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                                                                                             STRAIN=C6
                                                                                                                                                                                                              Autographa californica r
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                         Probable
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                                                                                                                      SEQUENCE
                                                                                                                                                                                            Nucleopolyhedrovirus.
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194 240 A
242 269 A
262 267 PP
272 334 H
373 390 P
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K -> Q (IN MEIS1-2).
F -> L (IN MEIS1-2).
E -> K (IN MEIS1-2).
N -> H (IN MEIS1-2).
G -> K (IN MEIS1-2).
MISSING (IN MEIS1-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQPSYTTSQMPLHHAQLRHGTSVHTYIPGHHHHPAMMMHGG PPQPGMPISASSPSVLNTGNDSMSCGUVVVVVV
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PMSGMGMNMGMEGQWHYM ->
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                    Autographa
                                                                                                                                                                                                                polyhedrosis virus (ACMNPV).
stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D0D98637D08CF32F CRC64;
                                          Lopez-Ferber M.,
                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                               506
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Best Local
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                                                                                                                                           BRF3_HUMAN STANDARD
Q9ULDA;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
15-JUN-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               15-JUN-2002 (Rel. 40, Last sequence update)
Bromodomain and PHD finger-containing protein BRPF3 OR KIAA1286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
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SMART; SMO
Helicase;
                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00176; SNF2_N; 1.
Pfam; PF00271; helicase_C;
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyhedrosis virus.";
Virology 202:586-605(1994).
-i- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
            MEDLINE-20039619; PubMed-10574462; Nagase T., Ishikawa K.-I., Kikuno
                                                                                       EMBL;
                                     TISSUE-Brain
                                               SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=9606;
                                                                                    Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001650; Helicase_C. InterPro; IPR000330; SNF2_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity 22.3%;
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                                                                                                                                                                                                                                                                               KRKQQHNLS 380
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                                                                                                                                                                                                                                                                                                                                                                            -----FQS--ESSTPSTGGFSGK------ETPSEDDRSQSREHMGESLSLKAGG
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157
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                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                             -LLPP--SPKVEKKDPSRKKEWWENAGNKIYTM--AADKTISKLMTEYK
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           Kikuno R.,
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Pred. No. 2.7;
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                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae
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protein
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             Nomura
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Best Local
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DOMAIN
SEQUENCE
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for large proteins in vitro.";
DNA Res. 6:337-345(1999)
-1- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-1- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC
-1- SIMILARITY: CONTAINS 1 PHOP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00628; PHD; 1.
Pfam; PF00855; PWWP; 1.
PRINTS; PR00503; BROMODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB033112; BAA86600.1; -. HSSP; Q92831; 1B91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001487; Bromodomain.
InterPro; IPR000313; PWWP_domain.
InterPro; IPR001965; Znf_PHD.
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876
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SM00293; PWWP;
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HGNC:14256; BRPF3
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                                             DPSR-----KKEWWENA----GNK-IYTMAADKTISKLMTEYKKRKQQHNLSAFPKE
                                                                                                  AVLEQALQEEPEDDGDRDDSKLPPPPTLEPTGPAPSL----SEQESPPEPPTLKPINDSK
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PPSRFLKPRKVEEDELLEKSPLQLGNEPLQRLLSDNGINRLSLMAPDTPAGTPLSGVGRR
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                                                                                                                             -KETPSED-DRSQSR-----EHMGESLSLKAGGGDLLLPPSPKV----EKK
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ZF_PHD_2;
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685
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BROMODOMAIN_2;
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22.5%;
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GLU-RICH.
BROMODOMAIN.
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Pred. No. 8.
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01-NOV-1997
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Pfam; PF03221; Transposase_Tc5; 1.

SMART; SM00299; CLH; 1.

SMART; SM00184; RING; 1.

SMART; SM00184; RING; 1.

PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

PROSITE; PS0089; ZF_RING_2; 1.

HYDOTAL TOTAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (SEP-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: REQUIRED SIMILARITY).
-!- SIMILARITY: BELONGS
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WormPep; F32A6.3; CE29305.
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                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                          Hypothetical
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001841; Znf_ring.
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15-JUN-2002 (Rel.
15-JUN-2002 (Rel.
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                                                                                                                                                            66; Conserv
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an email to license@isb-sib.ch).
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                               ACLFNNVKQFRKLVQTWSPDLYMTSFIIDRTQWRIQQISKSGNLADVDETERVLMDALAH
    FLRY--
                                                                SLLSHQV----
                                                                                              RARAAASRLPLICGECKEEWEWAVNQFEEVKLCTLLAEVLPDGTP---
                                                                                                                           RIRAMAQQVFMLDTQCSPK---TPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVV
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IPR004906; Transposase_Tc5.
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814 868
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CONTAINS 1 RING-TYPE ZINC FINGER.
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99987 MW;
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                                                                                                                                                            64;
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VACUOLAR ASSEMBLY AND VACUOLAR TRAFFIC
                                                                                                                                                                         Score 104.5; I
Pred. No. 6.2;
                                                                                                                                                                                                                                          RING-TYPE
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InterPro; IPR001140; ABCtranprtrTM.
InterPro; IPR005292; MRP_assoc.
                                                           EMBL; AB010466; BAA28954.1;
EMBL; U73038; AAD12747.1; -.
HSSP; P13569; 1NBD.
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PF00005;
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                       Madon J., Hagenbuch B., Stieger B., Meier P.J.;
"Cellular localization and functional characterization of a not
liver multidrug resistance-associated protein (mrp6).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PARTICIPATE DIRECTLY IN THE ACTIVE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; MEDLINE=98279126; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE=Liver;
Madon J., Hagenbuch B., Stieger B., Meier P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                               DRUGS INTO SUBCELLULAR ORGANELLES OR INFINDIRECTLY (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane
TISSUE SPECIFICITY: HIGH IN LIVER AND LO
                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atic expression of multidrug resistance-associated eins maintained in eisai hyperbilirubinemic rats.", Pharmacol. 53:1068-1075(1998).
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                                            an email to license@isb-sib.ch)
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126; PubMed-9614210;
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PROSITE; PS00211; ABC_TRANSPORTER; 2.
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CYTOPLASMIC (BY SIMILARITY).

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EXTRACELLULAR (BY SIMILARITY).

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CYTOPLASMIC (BY SIMILARITY).

16 (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).

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12 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

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EXTRACELLULAR (BY SIMILARITY).

9 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

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17 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

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ATP (POTENTIAL).
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539901B674A74A28 CRC64;
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                                                                                                                                                                TLSLVISDAFRFAVPKLLSLFLEFMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1502;
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ABF1_MOUSE
     Pfam; PR00046; homeobox; 4.
Pfam; PF00096; zf-C2H2; 20.
ProDom; PD000010; Homeobox; 4.
SMART; SM00389; HOX; 4.
SMART; SM00355; znF-C2H2; 22.
SMART; SM00451; znF-U1; 7.
PROSITE; PS00027; HOMEOBOX_1; 2
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABF1_MOUSE
Q61329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/MK X ICR; TISSUE-Brain;
MEDLINE=96194902; PubMed=8654949;
MEDLINE=96194902; PubMed=8654949;
MEDLINE=96194902; PubMed=8654949;
MEDLINE=96194902; PubMed=8654949;
MEDLINE=96194902; PubMed=86549499;
MEDLINE=96194902; PubMed=86549499;
MEDLINE=961969; Industry Indust
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-fetoprotein enhancer binding protein (A'CAT-binding transcription factor 1).
                                                                                                                                                                                                                                                                                                                            Transcription DNA-binding; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001356; Homeobox.
InterPro; IPR000822; Znf_C2H2.
InterPro; IPR003604; Znf_U1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T03881; -- MGD; MGI:99948; Atbf1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D26046; BAA05046.1; -. HSSP; P20263; 10CP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we see by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: Transcriptional activator that binds to the sequence of the enhancer element of the AFP gene.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: CONTAINS 4 HOMEOBOX DOMAINS.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                             PS50071; HOMEOBOX_2; 4.
PS00028; ZINC_FINGER_C2H2_1; 15.
PS50157; ZINC_FINGER_C2H2_2; 9.
Ption regulation; Activator; Zinc
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Rodentia;
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C2H2-TYPE.
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AT-rich core

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Job time: 34.0952 secs
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                                            1396 AKRPQ 1400
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                                                                                       1351 ----GGDL-----KPTSADPSCGREDSGFLCWKKGCNQVF-----KTSATLQTHFNEVH 1395
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                                                                                                      320 LKAGGGDLLLPPSPKVEKKDPSRKKE-----WWENAGNKIYTMAADKTISKLMTEYK--- 371
                                                                                                                                  1297 MTVTAPEMVMPSSMFLPAAAADRDGNSTLEEVGKQPEASEDPGKNILPPASMEH----- 1350
                                                            372 -KRKQ 375
                                                                                                                                               234 SNADWVWIJVKRLH------KICMELCNN--YIQMHLD-----LENCMEEPP 271
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406567 MW; 915ACBE588A72C98 CRC64;
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HOMEOBOX 4.
C2H2-TYPE.
C2H2-TYPE.
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HOMEOBOX 2.
C2H2-TYPE (ATYPICAL).
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                    and is derived by analysis of the total score distribution.
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
      /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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US-09-738-626-4700

US-09-982-091A-4

US-09-982-3187-88

0 US-09-764-864-823

0 US-09-764-864-1161

US-09-764-864-11574

US-10-151-599-2

US-10-171-311-113

US-09-823-187-87

US-10-133-68-468

US-10-133-68-468

US-10-133-357

0 US-09-801-368-208
                                                                                                                                                                          US-09-836-499-2

US-10-162-435-2

US-09-836-499-5

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0 US-09-788-600-5
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US-09-816-669A-14
                                                                                                                                                                                                                                                                                                                                           SUMMARIES
          Sequence 4700, Ap
Sequence 88, Appli
Sequence 88, Appl
Sequence 823, App
Sequence 1161, Ap
Sequence 1574, Ap
Sequence 2, Appli
Sequence 87, Appl
Sequence 87, Appl
Sequence 468, Appl
Sequence 377, Appl
                                                                                                                                                                       Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                  Sequence 28
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                   printed,
                                                                                                                                                                                                                                                  Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08681219
Patent No. US20020058607A1
GENERAL IMFORMATION:
APPLICANT: Takaaki Sato and Junn
```

	ALIGNMENTS				
56			3.4	91.5	5
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Sequence 27, Appl	10 US-09-821-883-27		3.4	92	3
Sequence 32, Appl	8 US-08-681-219-32		3.4	92.5	2
Sequence 2, Appli	10 US-09-904-380-2		3.4	92.5	4.1
Sequence 282, App	10 US-09-801-368-282		3.4	92.5	0
Sequence 19, Appl	10 US-09-745-763-19		3.4	92.5	39
Sequence 425, App	10 US-09-738-973-425		3.4	93	38
Sequence 425, App	9 US-09-854-133-425		3.4	93	37
Sequence 2, Appli	10 US-09-908-500A-2		3.4	93	36
Sequence 2, Appli	9 US-10-154-386-2		3.4	93	ü
Sequence 4, Appli	9 US-10-029-217A-4		3.4	93	34
Sequence 1094, Ap	10 US-09-925-301-1094		3.4	93 .	3
Sequence 1934, Ap	9 US-10-017-754-1934		3.4	93	32
Sequence 1934, Ap	9 US-09-902-941-1934		3.4	93	31
Sequence 37015, A	10 US-09-864-761-37015		3.4	93	30
Sequence 58, Appl			3.5	93.5	29
Sequence 7, Appli	9 US-09-987-107-7		ა . 5	93.5	28
Sequence 12173, A	10 US-09-815-242-12173	300	ω. 5	94	27
5680,	10 US-09-815-242-5680		3.5	94	26
220,	10 US-09-771-161A-220		ω . 5	94.5	25
	10 US-09-771-161A-219		3.5	94.5	24
Sequence 678, App	9 US-10-102-806-678		3.5	94.5	23
Sequence 4, Appli	10 US-09-954-043-4		ა	94.5	22
4	⊐	907	3.5	94.5	21
Sequence 1282, Ap	10 US-09-764-864-1282		3.5	94.5	20

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; MOLECULE TYPE: US-08-681-219-28
                                                                                                                                          TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATION
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: LILL
STREET: New York
CITY: New York
TIS.A.
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 828 amino acid
                                                                                                                                                                              TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BI
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                    STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
                                                                        amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                    ss: single
linear
                 peptide
                                                                                                                                                                                                                                              28,678
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RESULT 2
US-09-816-669A-14
; Sequence 14, Application US/09816669A
; Patent No. US20020137019A1
                                                                                                                           ; ORGANISM: Human US-09-816-669A-14
                                                                                                                                                                                    SEQ ID NO 14
LENGTH: 2783
                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/225,618 PRIOR FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GARABEDIAN-1.1A CURRENT APPLICATION NUMBER: US/09/816,669A CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARKUS, Steven
TITLE OF INVENTION: METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF
TITLE OF INVENTION: TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL
TITLE OF INVENTION: PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES
                                                                                                                                                                 LENGTH: 27
TYPE: PRT
                                                                                                                                                                                                                              SOFTWARE: PatentIn
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GARABEDIAN, Michael APPLICANT: TANEJA, Samir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                            Local
132 KCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLT--
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                                            73; Conserv
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18.48;
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                                       Score 108.5; D
Pred. No. 6.5;
Nismatches
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                                     91;
                                       Indels 145;
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NQETIT 174
                                       Gaps
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US-09-836-499-2
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Best Local Sim
Matches 111;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09836499 Publication No. US20030027316A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 16051A AND 16051B, NOVEL
TITLE OF INVENTION: FAMILY MEMBERS AND USES
FILE REFERENCE: 10448-043001
CURRENT APPLICATION NUMBER: US/09/836,499
CURRENT ETLING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/197,507
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1294
                                                                                                                                                                                  1007
                  1093 FVQM--EKESCSH-----LKSDLVRIKRLFPGQPAEENGAIAAGDIILAVNGRSTEGLIFQ 1146
                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                             893 SLLSHTQDQDRNTEELDMAGVQSLVPRLRHQLSFLPLKGAGSSCPPSPPEISAGEIYFVE
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                                                        YIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMG
                                                                                                  SMGDERTAVS---
                                                                                                                                        DIFEETAQVSPPRGKEKRQWRARMPLLSVQP-----VSNADWVWLVKRLHKLCMELCNN
                                                                                                                                                                                                                     NLYRQSAMSFNIYFHALVCAVLTNQETITA----EQVKKVLFEDDERSTDSSQQCSSEDE
                                                                                                                                                                                                                                                               LVKEDGTLGFSVTGGINTSVPYGGIYVKSIVPGGPAAKEGQILQGDRLL--QVDGV----
                                                                                                                                                                                                                                                                                                         LA---GFLRY----
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                                                                                                                                                                             ILCG-LTHKQAVQCLKGPGQVARLVLE--RRVPRSTQQCPSAND
                                                                                                                                                                                                                                                                                                                                                                                  -----QVLLQNLYDILLEEFVKG-----PSPGEEKTIQVPEAK 95
                                                                                                ------LYTALPGRPSSCVSVTDGPKFEVKLKKNANGLGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
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Pred. No. 11;
66; Mismatches
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US-10-162-435-2

Sequence 2, Applicat Publication No. US20 GENERAL INFORMATION:

Application US/10162435 No. US20030096305A1

APPLICANT: APPLICANT:

Curtis , Rory A. Bandaru, Rajasekhar Kapeller-Libermann, Rosana Glucksmann, Maria Alexandra

Rachel

APPLICANT:

FILE REFERENCE:

10448-189001

FILING DATE: 2001-04-17
APPLICATION NUMBER: US 60/197,507

FILING DATE:

2000-04-18

APPLICATION NUMBER: US 09/891,008 FILING DATE: 2001-06-25

FILING DATE:

FILING DATE:

2001-06-25

FILING DATE:

APPLICATION NUMBER: US 09/860,868 APPLICATION NUMBER: US 60/214,220

2001-05-18 2001-05-18 2000-06-23

APPLICATION NUMBER: US 09/836,499

2001-04-1

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CURRENT APPLICATION NUMBER: US/10/162,435
CURRENT FILING DATE: 2002-06-04
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TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
TITLE OF INVENTION: CELL SURFACE PROTEIN FAMILY MEMBERS
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US-09-836-499-5
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Best Local Similarity
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CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/197,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 16051A AND 16051B, NOVEL HUMAN PDZ TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF FILE REFERENCE: 10448-043001
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
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TYPE: PRT
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893 SLLSHTQDQDRNTEELDMAGVQSLVPRLRHQLSFLPLKGAGSSCPPSPPEISAGEIYFVE
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                                        58 SLLSH-----
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; ORGANISM: Homo sapiens US-10-162-435-2

SEQ ID NO 2

FastSEQ

FILING DATE:

2000

-08-21

60/226,612

APPLICATION NUMBER: US

APPLICATION NUMBER: PCT/US01/41811 APPLICATION NUMBER: US 09/934,268 FILING DATE: 2001-08-21 APPLICATION NUMBER: US

60/260,286

2001-01-08 2002-01-08 2002-01-08

ICATION NUMBER: PCT/US02/00275

APPLICATION NUMBER: US 60/213,963 FILING DATE: 2000-06-23

2001-06-21

APPLICATION NUMBER: US 09/886,429 APPLICATION NUMBER: US 60/205,674

2001-06-21 2000-05-19

APPLICATION NUMBER: US

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US-10-162-435-5
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                                                                                         FILING DATE: 2001-06-21 APPLICATION NUMBER: US 60/213,963
                                                                                                                                                                    FILING DATE: 2000-05-19
APPLICATION NUMBER: US 09/886,429
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                                                    NUMBER: US 10/041,406
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US-10-162-435-5
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US-09-788-600-5
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                                                                                                                                                                                                            Sequence 5, Application US/09788600 Patent No. US20020004489A1 GENERAL INFORMATION:
FILE REFERENCE: PT017P1

FILE REFERENCE: PT017P1

CURRENT APPLICATION NUMBER: US/09/788,600

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: PCT/US00/22351

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 60/189,026

PRIOR FILING DATE: 2000-03-14
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APPLICATION NUMBER: US
FILING DATE: 2001-01-08
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Pred. No. 11;
66; Mismatches
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US-09-738-626-4700

Sequence 4700, Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION:
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PRIOR FILLING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
 SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4700
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                                              CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                        APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
                                   PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
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ORGANISM: Homo sapiens
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Local Similarity 19.1%; Pred. No. 3.
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                           MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                             HAYASHI,
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RESULT 9
US-09-982-091A-4
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                                                                                                                                                                                                                                                                                US-09-982-091A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: KUMAGAI, AKIKO
APPLICANT: DUNPHY, William
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS
                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4
LENGTH: 1332
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09982091A Patent No. US20020151030A1
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Matches 96; Conserv
                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                            LENGTH: 13
TYPE: PRT
                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                     Local Similarity 20.4 hes 73; Conservative
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                                           PLLSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLEN-----CMEEPPIFKGDPF 278
                                                                                           SDEEIFVSKKLKNRKVLQDSDSETEDTNASPEKTTYDSAEEENKENLYAGKNTK-----
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21.1%; Pred. No.
                                                                                                                                                                                                          3.6%; Score 98; DB 20.4%; Pred. No. 18;
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US-09-823-187-88
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                                                                                                                                                          ; ORGANISM: Mus musculus 
US-09-823-187-88
                                                                                                                                                                                              SOFTWARE: Pat
SEQ ID NO 88
LENGTH: 669
TYPE: PRT
                                                                        Query Match 3.6
Best Local Similarity 18.6
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/823,187
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                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/193,205
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/197,525
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60 FILING DATE: 2000-04-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/195,792
                      184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPR-----GKEKRQWRARMPLLSVQPVSNADW 238
186 EEDSESPSESEKTSDQDFTPEKKTA-ARPPRRGPLGGRKKKK------VPSASDSD- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 SLSVSVRDAEAQIQAWTNMVL--TVLNQIQILDD----QTFTALQPAVFPCISQLTCH 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 FPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 MEKIRQLKKKETKNQEDDVEQPFNDSGCLLVDKDLFETGLEDENNSPLEDEESLESIRAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 VEKKDPSRKKEW-----WENAGNKIYTMAADKTISKLMTEYKKR---KQQHNL----SA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 ---LSLQSGNSTDFT------TDRKSSKKHIHDKEGTAGKAKVKSKRRLEKEERK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 FILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHM----GESLSLKAGGGDLLLPPSPK 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Taupier, Raymond J
INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
RENCE: 1596-745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION NUMBER: 60/195,005
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Shimkets, Richard A
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                                                                          57;
                                                                                            Score 97.5; D. Pred. No. 7.4;
                                                                          Mismatches
                                                                                                                 DB 9;
                                                                          125;
                                                                                                                 Length 669;
                                                                          Indels 163;
                                                                          Gaps
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3.6%; Score 96.5; DB 10; Length 759; ty 19.1%; Pred. No. 11; ervative 84; Mismatches 184; Indels 159; Gaps 26;	Similarity 1; Conserv	Query Match Best Local : Matches 10	
: Xaa equals any of the naturally occurring L-amino acids	ION:	LOCATI OTHER -09-764-	SI
: Xaa equals any of the naturally occurring L-amino acids		OTHER INFO	
: Xaa equals any of the naturally occurring L-amino acids	••	OTHER INFO	
: Xaa equals any of the naturally occurring L-amino acids			
: Xaa equals any of the naturally occurring L-amino acids	(18) RMATION: SITE	~	•
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N) C	S20020132 RMATION: Rosen et	NO. L INF	
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RPVKVERTRKRSEGLSLERKGEKKKEPSVEERLQKLH 47	QKEKRGRPDI	4	ğ ;
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Ğ	SSSSSSDSDV	b 262	$\ddot{\sigma}$
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84 G---EEKTIQVPEAKLAGFLRYISMQNLAVIFDLL--LDSYR-----TAREFDTSPGLK 132

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1161
LENGTH: 555
TYPE: PRT
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
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Best Local Similarity
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Pred. No. 7
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US-09-764-864-1574
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1574
LENGTH: 555
TYPE: PRT
                                                                                                                                                                                                                       Sequence 2, Application US/10151569
Publication No. US20030040050A1
GENERAL INFORMATION:
                             SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2 LENGTH: 693
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Best Local
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                                                                                                                                         CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2002-05-20
                                                                                                                                                                          APPLICANT: Matsumoto, Kunihiro TITLE OF INVENTION: NOVEL PROTEIN TAB2 FILE REFERENCE: 06501-110US1
                                                                                     NUMBER OF SEQ ID. NOS:
                                                                                                    PRIOR APPLICATION NUMBER: PCT/JP99/06466 PRIOR FILING DATE: 1999-11-19
   ORGANISM: HOMO
                  TYPE: PRT
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Pred. No.
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APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KI
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
                                                    CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                        APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
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                                                                                                                                                                                                                                                                      Monahan, John
Kamatkar, Shubhangi
Glatt, Karen
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; SEQ ID NO 113

; LENGTH: 1713

; TYPE: PRT

; ORGANISM: Homo sapiens

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                                                                        KHLCVYLEAGKVTASMDSGAGGTSTSVTPKQSLCDGQ-WHSVAVTIKQHILHLELDTDSS
                                                                                                                                                                                                                                 DGLRARE-GSLPGNSTISIRAPVYLGSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSS 152:
                                                                                                                                                                                                                                                                                                                FALGTDGKKL-----RIKSKEKCNDGKWHTVVFGHDGEK-----GRLVV------
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YTAGQIPFPPASTQEPLHLGGAPANLTTLRI 167:
                                   FTALQPAVFPCISQLTCH-----VTDIRV 499
                                                                                                                                                       SFGVSSCLGGPLEKGIYFSEEGGHVVLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPG
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ative 84; Mismatches
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Search completed: June 17, Job time : 58.3646 secs 2003, 12:02:27

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A;Description: Analysis of the nucleotide sequence
A;Reference number: S56186
A;Mocession: S56274
A;Molecula *****
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A; Residues: 1-2278 <MUR>
A; Residues: 1-2278 <MUR>
A; Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09258.1;
R; Yamamoto, A.; Koshland, D.
submitted to GenBank, August 1993
A; Description: FAB1: a novel gene required for endocytic-vacuol A; Reference number: A55997
A; Accession: A55997
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C; Superfamily: FAB1
F; 1911-2266/Domain:
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A;Residues: 1-2274,'R',2276-2278 <YAM>
A;Cross-references: GB:U01017; NID:g392993; PIDN:AAA81360.1; PID:g398498
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       228 LSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCME-----
                                                                                                                                                                                                                                                                           108;
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                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                         -LYYKILEKINNFYGSVLSRLERIKLDSMTKDKV-----LSGQAKIIELKSNATEEQK 1434
                                                                                                                                                                                                                                    KTPNNF--DHAQSC---QLIIEL-------PPDE---KPNGHTKKSVSFREIVVS
                                                       KCPHDFTKDHVKYFGYNDLVVRLEYSDLEVHELITPPRKIKWKPHIDIKLKVE-----
                                       TDISRITAKOLKKLFY------DSSRKDSEDKKSLHDEKAKTRKPEKNE------LPL
                                                                                                LMLQDLDTFYADSPCDQHLPLNLVIK-----SLY-DKAVNWNSTFAIFAKSYLPSE 148.
                                                                                                                            L----LDSYRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVL--- 167
                                                                                                                                                                                   LLSHQVL--LQNLYDILLE--EFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDL
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 1-phosphatidylinositol-4-phosphate 5-kinase
1-phosphatidylinositol-4-phosphate 5-kinase homology
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                                                                                                                                                                                                                                                                                        Score 126; DB 1; Length 2278; Pred. No. 0.98;
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                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, T.; Ozawa,
                                                                                                                                                                                                                                                                           148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of chromosome
                                                                                                                                                                                                                                                                           Indels 170;
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RUD3 protein - yea
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S.I.;

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114 1382

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Query Match 214: Conservative 20.6%; bred. No. 1.3;  Best Local Similarity 20.6%; bred. No. 1.3;  Matches 114: Conservative 63; Mismatches 166; Indels 210; Gaps 24;  Qy 33 IIELPPDEKDNGHTKKSVSFREIVVSLLSHOVILQNLYDILLEEFVK 79;	PLHSRSSGNNLSSANVKTLEAPV 1729  PLHSRSSGNNLSSANVKTLEAPV 1729  rotein - Caenorhabditis elegans enorhabditis elegans e	Qy 276 DPFFILPSFQSE-SSTPSTGGFSGKETPSEDDRSQ-SREHMGESLSLKAGGGDLLLPPSP 333
Qy  80 GPSPGEEKTIO-VPEAKLAGELRYISMONLAVIEDLLLDSYRTAREEDTSPGLKC 133	T19450  Typothetical protein C25D7.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000 C;Accession: T19450 R;Ainscough, R. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19125 A;Accession: T19450 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-2150 <#MIL> A;Cross-references: EMBL:Z81039; pIDN:CAB02774.1; GSPDB:GN00023; CESP:C25D7.3 A;Experimental source: clone C25D7 C;Genetics: A;Gene: CESP:C25D7.3 A;Apa position: 5 A;Introns: 70/1; 102/1; 153/3; 258/1; 305/1; 1283/1; 1398/1; 1703/2; 1853/1; 1887/1; C;Superfamily: zinc finger protein sdc-3 Query Match Best Local Similarity 20.6%; pred. No. 1.3; Matches 114; Conservative 63; Mismatches 166; Indels 210; Gaps 24; Db 1177 IERLSEDQLLGDQGSEDISFEEIQVDLLLESGVEVQVNQSVTISRSSTSFEESLLVEDPEE 1236	Qy 360 DKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPR 398

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RESULT 5
741551
Pypothetical protein SPCC70.05c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: 741551
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z22001
A;Accession: 741551
A;Accession: 741551
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-781 <WOO>
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A;Molecule type: DNA
A;Residues: 1-482 <WIL>
A;Cross references: EMBL:Z48716; PIDN:CAA88601.1; GSPDB:GN00020; CESP:F59B10.
A;Experimental source: clone F59B10
C;GenetLcs:
A;Gene: CESP:F59B10.2
A;Map position: 2
A;Introns: 40/2; 74/1; 118/3; 415/1
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                                 EKNESLTEHPRSTELPKTHIEQIQKHFSEDNNEMIPMECDSFCSDQNES---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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A;Cross-references: EMBL:AL023794; PIDN:CAA19355.1; GSPDB:GN00068; SPDB:SPCC70.05c
A;Experimental source: strain 972h-; cosmid c70
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                            249 CMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPST-----GGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 STDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKRLHKL
                                                                                                                                                                                                                                                                         159 LHKNTSSHPSSPVNGKS--SDIHKSQSYQHLKNS------PPNSRTARKPVPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 TTDSMAHVPGNNSPL--QTPQKSPPRQKH-----TAPATPI-PVS-----ASRHHK- 116
                                                                                                                                                                                                                           KEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVK--VEKKGEPLGPRGQ-
PLVSRVRDNYANTSYESWPHSTEFDMFTYAVSGSLKLTPQGTGFDCINPA
                                             -LSVSVRD--AEAQIQAWTN------WVLTVLNQIQILPDQT-FTALQPA 482
                                                                                          RNREGGNGSYFDGPLTASPTPSSPTG-TPNSMSKSPSL-----SSLÅSTGASYRPGPSK
                                                                                                                                                                                ----ANSASHNLGSTKSPNGNAKESLSRSAELPSKAKPMEINNGYRKKPSPLSPNSSI
                                                                                                                                                                                                                                                                                                                                                                   -----PHHSGLKNLLEKA------MHPGHKSNANSPTSESPSKGFGSFINNHI 158
                                                                                                                                   -DSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.18;
                                                                                                                                                                                                                                                                                                 --SGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 111;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 118;
    361
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A; Molecule type: mRNA A; Residues: 1-1148 <AHA> A; Cross-references: EMBL: AF030234; A; Experimental source: HeLa cells C; Keywords: pre-mRNA splicing A;Title: Sip1, a novel RS domain-containing protein essential A;Reference number: 216554; MUID:98107652; PMID:9447963 A;Accession: T09073 A;Status: preliminary; translated from GB/EMBL/DDBJ 213 QISGLSQSEVKTDV-CTVHLPNDFPTCLTSESKVYQPVSCPLSDLSENVESVVNEEKITE 168 TNQETIT------AEQVKKVLFEDDER--STDSSQQCSSEDEDIFEETAQVSPP 58 SLLSHQVLLQNLYDILLEEFVKGP----SPGE-----EKTIQVPEAKLAGFLRYISMQN IATCDTFGNEDFNNIQDSENN-----LLKN-LAVIFDLLLDSYRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVL SSLV-EITEHKDFTLKTEELIESPKLESSEGEIIQTVDRQSVKSPEVQLLGHVETEDVEI 330 4.18; 78; Score 111; Pred. No. 5 NID: g2822459; PIDN: AAC39565.1; PID: g2822460 Mismatches DB 2; 183; Length 1148; Indels 154; for NLLNTKLEKSLE pre-mRNA splicing Gaps 213 367 167 107 57 271 20

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colorectal tumor suppressor protein - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:128163; OMIM:159350 A;Map position: 5q21-5q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-829 < KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kinzler, K.W.; Nilbert, M.C.; Vogelstein, B.; Miyoshi, Y.; Nishisho, I.; Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: MCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:M62397;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
     QRLDLENAVLMQELMAMKEEMAELKAQLYLLEKEKK-----ALELKLSTREAQEQAY
                                                  SPL-LORP---QHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                   DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKRL
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                                                                                                                                                   ADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKG-----
                                                                                                                                                                                                 LKRAHDCRKTAENAAKALLMKLDGSCGGAFAVAGCSVQP-----
                                                                                                                                                                                                                                                                                               SEQCIEAYELLL------ALAESEQSLILGQFRAAGVGSSPGDQSGDENITQM
                                                                                                                                                                                                                                                                                                                                             HKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKETPSE-
                                                                                                                                                                                                                                                                                                                                                                                                ETERLNSRIEHLKSQNDLLTITLE-----ECKSNAERMSMLVGKYESNATALRLALQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EISSIGVSSSVAEHLAHSLQDCSNIQEIFQTLYSHG------SAISESKIRE--FEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVSGIGGAANLYROSAMSF------NIYFHALVCAVLTNQETITAEQVKKVLFED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSPGEEKTI----QVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSRERESDRDGQR----RERERRTRKWS
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                                                                                                                                                                                                                                            ----DDRSQSREHMGESLSLKAGG--GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESLSLKAGGGDLLLPPSPKVEKKDPSRK-----KEWWENAGNKIYTMAADKTISKLMTE
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                                                                                                   -RLKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 110;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198;
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                                                                                                                                                 -----EPLG----PRGQD
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  A41948
alpha-fetoprotein enhancer-binding protein - }
N;Alternate names: ATBF1 protein
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec
C;Accession: A41948
R;Morinaga, T.; Yasuda, H.; Hashimoto, T.; Hi
Mol. Cell. Biol. 11, 6041-6049, 1991
Mol. Cell. Biol. 11, 6041-6049, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멍
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A; Residues: 1-587 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T24103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP:R102.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone R102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSVQPTLEDDMTQKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS-----EDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSQQCSSEDEDIFEETAQVSPPR----GKEKRQWRARMPLL-SVQPVSNADWVWLVKRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKLIKLVK -- EGETNNLKQGSKLEDDL -- TMSCGSLI------ VKRGATIETNFNNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVKG---PSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTA--REFDTSPGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MAADKTISKLMTE---YKKRKQQHNLSAFPKEVKVEKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMDQFDNEEAAVIEDLVQLKRSKEEKEKKKKKKKTKERMDALDELTHVTSNDRISLLSR--
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                                                                                                                                                                                                                                                                                                                                               --PRGQDSP-----LLQRPQHLMDQGQMRHSFSAGPELLRQDKR
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Pred. No. 2.
  enhancer-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 132;
                                                                                                31-Dec-1993 #text_change 15-Oct-1999
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                                                  Higashio,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 15-Oct-1999
protein,
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                                                Tamaoki,
  ATBF1,
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F;1618-1638/Region: z
F;1728-1784/Domain: l
F;1799-1820/Region: z
F;2033-2089/Domain: l
F;2013-2089/Domain: l
F;2112-2134/Region: z
F;2545-2565/Region: z
F;2585-2607/Region: g
F;2651-2633/Region: z
F;2650-2737/Region: s
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F;176-198/Region: zinc
F;311-332/Region: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C: Keywords: DNA binding: homeobox; nuc F;72-94/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2783 <MOR>
A;Cross-references: GB:D10250; GB:D90395; NID:g219429; PIDN:BAA01095.1; PID:g219430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A41948;
A; Accession: A41948
A; Molecule type: mRNA
global transactivator orf42 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
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F;1416-1437/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1117-1211/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;340-361/Region: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;1232-1288/Domain:
;1329-1385/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: alpha-fetoprotein enhancer-binding protein; Keywords: DNA binding; homeobox; nucleus; transcription i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-150/Region: zinc finger CCHH motif

5-198/Region: zinc finger CCHH motif

1-312/Region: zinc finger CCHH motif

361/Region: zinc finger CCHH motif

3-471/Region: zinc finger CCHH motif

3-509/Region: zinc finger CCHH motif

5-509/Region: zinc finger CCHH motif

6-55/Region: zinc finger CCHH motif

6-655/Region: zinc finger CCHH motif

3-605/Region: zinc finger CCHH motif
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                                                                                                                                                                                                                 376
                                                                                                                                                                                                                                                  275
                                                                                                                                                                                                                                                                                        320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 AEQVKKVLFEDDE-----RSTD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 KHLQQHESGVEGE-----SCYYHCVLCNYSTKAKLNLIQHVRSMKHQRSESLRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 KCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLT------NQETIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                  GDPFFILPSFQ-SESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAG---GGDLLLP
                                                                                                                                                                                                                                                                                                            LORLOKGLPEEDEDLGQIFTIRRCPSTDPEEAIEDVEGPSETAADPEELAKDQEGGASSS 266
                                                                                                                                                                         PSPKVEKKDPSRKKE----WWENAGNKIYTMAADKTISKLMTEYK----KRKQ 375
                                                                                                                                                                                                             TTPEMVMPSSMFLPAAVPDRDGNSNLEEAGK--QPETSEDLGKNILPSASTEQSGD--LK
                                                                                                                                                                                                                                                                                        D----VNRLRVHAMTQHSVQPMLRCPLCQDMLNNKIHLQLHLTHLHSVAPDCVEKLIMTV 375
                                                                                                                                                                                                                                                                                                                                                              QAEKELTDSPATSKRISFPGSSES------PLSSKRPKTAEEIKPEQMYQCPYCKYSNA 319
                                                                                                                                                                                                                                                                                                                                                                                                    QCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQP------
                                                                                                                                       PSP----ADPGSVREDSGFICWKKGCNQVF----
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i: zinc finger CCHH motif
i: homeobox homology <HOX4>
i: zinc finger CCHH motif
i: zinc finger CCHC motif
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homeobox homology <HOX2>
zinc finger CCHC motif
zinc finger CCHH motif
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serine/threonine-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 108.5;
20.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUID:92049333; PMID:1719379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                     -KTSAALQTHFNEVHAKRPQ 476
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regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                  ----- VSNA 236
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                                                                                                                                                                       A; Map position: A; Introns: 48/3;
                                                                                                                                                                                                         C; Genetics:
A; Gene: CESP: ZK154.5
                                                                                                                                                                                                                                                                                                                                                        A; Description: The sequence
A; Reference number: Z20119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-506 < KAM>
                                                                                                                                                                                                                                                                                                                                            A; Accession: T25985
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Best Local Similarity 21.6
Conservative
                                                                                                 Matches
                                                                                                               Query Match
Best Local
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                   190 LAKVAVIRAANVQKILEKRSLGKISTGGQAAAQDEEIFRYVTSNGNSELLNKMPNRG---
                                                                                                               Similarity
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                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380
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C;Date: 03-Dec-1999 #sequence_revision of the genome of Bombyx mort nucleopolyhedrovirus. A;Title: Sequence analysis of the genome of Bombyx mort nucleopolyhedrovirus. A;Reference number: 220020; MUID:99281911; PMID:10355780
A;Recession: T41788
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1173 CCON>
A;Cross-references: EMBL:U70844; PIDN:AAB09095.1; GSPDB:GN00028; CESP:ZK154.5
A;Experimental source: strain Bristol N2; clone ZK154
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Connell, M. submitted to the EMBL Data Library, September 1996 a.Description: The sequence of C. elegans cosmid Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ZK154.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tcC;Accession: T25985
                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 DTSPGLKCLLKKVSGIGGAANLYR-QSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 VEYLKIFENFFKQKNIATLMYTG-QLKVEDRILAETTFNNAADTQHRILLLSIKCGGVGL 422
167 LTNQETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIF-----EETAQVSPPRGKEK 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRQIC---CHPYLAMHGRNLLETNDCFKMDYMSSKCKRVLDLVDDILNTSDDKIILVSQW 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLIGGNHIVMLEPHWNPQIELQAQDRISRMGQTKNTYVYKMLNVEDNSIEK----YIKQR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------LLPP--SPKVEKKDPSRKKEWWENAGNKIYTM--AADKTISKLWTEYKKRK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FQS--ESSTPSTGGFSGKETPSED------DRSQSREHMGESLSLKAGGGDL 327
                                                                                                                                                                  126/3; 163/1; 628/3; 833/3; 915/2; 1105/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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                                                       4.0%; Score 108; DE 22.2%; Pred. No. 8.8; ative 31; Mismatches
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                                                                                                           DB 2; Length 1173;
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                                                       Indels 116;
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»;Contains: lipovitellin I; lipovitellin II; phosvitin; yolk glycoprotein

C;Species: Gallus gallus (chicken)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-200

C;Accession: T29088; S55681
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A;Description: cDNA cloning and estrogen-induced expression (A;Reference number: Z20557
A;Accession: T29088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S55680; MUID:95322425; PMID:7599159
A;Accession: S55681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1912 <MAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: liver
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;Keywords: egg yolk; glycoprotein; liver; phospl
;1-15/Domain: signal sequence #status predicted
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Biophys. Acta 1244, 384-394,
                                                                                                      1147
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                                                                                                    ADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSE-----
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 EPIGPRGQDSPLLQRPQHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGS---SLSVSVRD
                                   SKSNRSSSSSNSKDSSSSSSKSNSKGSSSSSSSKASGTRQKAKKQSKTTSFPHASAAE--G
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                                                                    PKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKG
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1995
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                                                                                                                                                                      -QGDPQINLKSRQSKANEKKFYP
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RESULT 14
B72855

C; Species: Autographa californica nuclear polyhedrosis C; Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A; Note: dsDNA virus
C; Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C; Accession: B72855
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C;Superfamily: peptide synthetase ppsD; acetate-CoA ligase homology; acyl carrier C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;1025/Binding site: phosphopantetheine (Ser) (covalent) #status predicted F;2068/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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A; Molecule type: DNA
A; Residues: 1-2617 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB74343.1; PID:g17131737; GSPDB:GN00179
A; Cross-references: GB:BA000019; PIDN:BAB74343.1; PID:g17131737; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakazaki, N.; Shimpo, S.;
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide synthetase [imported] - Nostoc sp.
C; Species: Nostoc sp.
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                                       GGFSGKETPSED
                                                                            DWTY-SKQLHHRQTIATLAENYQQILLSLIQHCL:
                                                                                                                    DWVWLVKRLH--KLCMELCNNYIQMHLDL-ENCMEEPPIFKGDPFFILPSFQSESSTPST
                                                                                                                                                                                                                                           GISLKAIKEQLRQIPDRGISYGLLRYLASP---
                                                                                                                                                                                                                                                                              SPGLKCL---LKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE 184
                                                                                                                                                                                                                                                                                                                        AFQTWTGENRLLVELEGHGREDLFPSINLSRTMGWFTS----LFPVLLDIYPSA---DL
                                                                                                                                                                                                                                                                                                                                                               G--PSPGEEKTI------QVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDGISWRVFLEDLQLAYQQLSQGQQIQLPPKTTSYQQWANKLQEHTWSADLQAAFNYWTS
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                                                                                                                                                                                                 DDERSTDSSQQCSSEDEDIFEETAQVSPPR---GKEKRQWRARMPLLSVQPV----SNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%;
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); Mismatches
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; Takazawa,
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M.; Yamada
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; Yasuda, N
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Tabata
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	379 RARAASRLPLICGECKEEWEWAVNQFEEVKLCTLLAEVLPDGTPTLDPECYQKVLI  58 SLLSHQVLLQNLY-DILLEEFV	
•	4.5; DB 2; 9.9; tches 138; HAQSCQLITELP	
736/1; 8	C;Genetics: A;Gene: CESP:F32A6.3 A;Introns: 31/2; 69/3; 111/3; 146/2; 247/3; 290/2; 352/3; 416/3; 632/3; 666/1;	
DESP:F32A6	;Molecule type: DNA ;Residues: 1-830 <wux> ;Cross-references: EMB ;Experimental source:</wux>	
	A; Description: The Sequence of C. elegans cosmid F32A6. A; Reference number: Z18483 A; Accession: T16236 A; Status: preliminary; translated from GB/EMBL/DDBJ	
	cal protein F32A6.3 - Caeno : Caenorhabditis elegans O-Sep-1999 #sequence_revisi on: T16236	
	::  :: 476 KQRQDKKIA	
a.	Qy 372 KRKQQHNLS 380	_
	Qy 325 GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371	
	Qy 284FQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGG 324 b 362 QWVEYLKIFENFFKQKNIATLMYTGQLKVEDRILAETTFNDAANTQHRILLLSIKCGG 419	_
	Qy 245 LHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPS 283    :-   :   :	
	Qy 185 DDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKR 244 :: :: :      :   :   :   :   :   :   :	
	Qy 126 DTSPGLKCLLKKVSGIGGAANLYR-QSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFE 184   :	_
	Query Match 3.9%; Score 105; DB 2; Length 506; Best Local Similarity 22.3%; Pred. No. 4.5; Matches 69; Conservative 49; Mismatches 91; Indels 100; Gaps 18;	
·	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-506 <ayr> A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66672.1; PID:g559111 C;Genetics: A;Gene: AC-GTA</ayr>	
is virus	R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994 A;Title: The contete DNA sequence of Autographa californica nuclear polyhedros A;Reference number: A72850; MUID:94303173; PMID:8030224 A;Accession: B72855	

	715 N 715	Db	
	292 S 292	Qy	
714	- ;	Db	
291	232 PVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTP 291	Qy	
664	HYDAVKMM	Db	
231	190TDSSQQCSSEDEDIFEETAQVSPPRGKE	Qy	
606		Db	
189	140 GIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFEDDERS 189	Qy	
555	DKHQLFDLVKDQITELM	Db	virus.
139	99 FLRYISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLKKVS 139	Qy	

Search completed: June 17, 2003, 12:01:08 Job time: 63.1151 secs

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is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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JH0148
A27441
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hypothetical prote
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nucleolin - mouse
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UL54 protein - hum
UL54 protein - hum
UL54 protein - hum
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conserved hypothet
related to TOM1 pr
hypothetical protein w
surface protein rh
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nucleolin - rat
nucleolin - Chines
unknown protein F1
UL54 protein - hum
SGT1 protein - yea
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44	43	42	41	40	39	38	37	36	ა 5	34	ω ω	32	31	30
544	54	54	54	54	54	54.5	54.5	54.5	55	55	55	55	55	55
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489 529	332	328	328	314	206	1070	899	440	1241	1040	765	731	426	411
20 20	N	N	Ν	N	Ν	N	Ν	Ν	N	N	2	N	N	N
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dentin matrix acid f42h10.7 protein -	endospore developm	hypothetical prote	hypothetical prote	probable C2H2-type	translation elonga	tolloid-BMP-1 like	hypothetical prote	transcription fact	potassium transpor	BEB1 protein - yea	hypothetical prote	nephrocystin - hum	hypothetical prote	peptidylprolyl iso

## ALIGNMENTS

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Query Match 29.6%; Score 64; DB 2; Length 707;	C;Superfamily: nucleolin; ribonucleoprotein repeat homology C;Keywords: DNA binding; nucleolus; nucleus; phosphoprotein; RNA binding F;308-373/Domain: ribonucleoprotein repeat homology <rrm1> F;394-456/Domain: ribonucleoprotein repeat homology <rrm2> F;487-550/Domain: ribonucleoprotein repeat homology <rrm3> F;573-634/Domain: ribonucleoprotein repeat homology <rrm4></rrm4></rrm3></rrm2></rrm1>	A; Residues: 231-236;349-362;399-403;458-461;655-656,'X',658-660 <jor> A; Experimental source: surface-labelled HeLa cells C; Genetics: A; Gene: GDB:NCL A; Cross-references: GDB:125908; OMIM:164035 A; Map position: 2012-20ter</jor>	A;Experimental source: HeLa cell nuclel A;Note: sequence extracted from NCBI backbone (NCBIP:134645) R;Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D. Biochemistry 33, 14696-14706, 1994 A;Title: Major cell surface-located protein substrates of an ecto-protein kinase are A;Reference number: A55996; MUID:95086063; PMID:7993898 A;Accession: A55996 A;Accession: A55996	R;Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R. Mol. Cell. Biol. 13, 4301-4310, 1993 A;Title: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G) an A;Reference number: A48138; MUID:93309464; PMID:8321232 A;Accession: A48138 A;Molecule type: protein A;Residues: 458-474 <ish></ish>	A;Cross-references: GB:M60858; GB:J05584, NID:g189305; PIDN:AAA59954.1; PID:g189306 R;Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L. FEBS Lett. 250, 99-105, 1989 A;Title: Cloning and sequencing of the human nucleolin cDNA. A;Reference number: S04631; MUID:89290043; PMID:2737305 A;Accession: S04631 A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-707 <sr2></sr2>	C;Accession: A3804; S04631; A48138; A5596 R;Srivastava, M.; McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L. J. Biol. Chem. 265, 14922-14931, 1990 A;Title: Genomic organization and chromosomal localization of the human nucleolin gen A;Reference number: A35804; MUID:90368666; PMID:2394707 A;Accession: A35804 A;Molecule type: DNA A;Residues: 1-707 <sri></sri>	RESULT 1 A35804 A35804 nucleolin - human N;Alternate names: phosphoprotein pp100; protein B50; protein C23 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man)

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A; Note: the authors translated the initiation codon GTG for residue 1 as Val R; Lischwe, M.A.; Cook, R.G.; Ahn, Y.S.; Yeoman, L.C.; Busch, H. Blochemistry 24, 6025-6028, 1985
A; Title: Clustering of glycine and Ng, Ng-dimethylarginine in nucleolar protein C23. A; Reference number: A24088; MUID:86104094; PMID:4084504
A; Accession: A24088
                                                                   R;Lapeyre, B; Bourbon, H.; Amalric, F.
Proc. Natl. Acad. Sci. U.S.A. 84, 1472-1476, 1987
Proc. Nucleolin, the major nucleolar protein of growing eukaryotic cells:
A;Title: Nucleolin, the major nucleolar protein of growing eukaryotic cells:
A;Reference number: A27441; MUID:87175501; PMID:3470736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 68, 73-84, 1988
A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization A;Reference number: I48118; MUID:89121496; PMID:2906027
A;Accession: I63130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 88, 187-196, 1990
A;Title: Nucleolin gene organization in rodents: highly A;Reference number: JH0148; MUID:90269607; PMID:2347493
A;Accession: JH0148
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A; Start codon: GTG
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A;Residues: 'MV',2-44 <RES>
A;Cross-references: GB:M22090; NID:g205793; PIDN:AAA41733.1; PID:g205794
C;Comment: This protein is the major nucleolar-specific protein in eukaryotic exponentia
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A; Residues: 1-712 <BOU>
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A; Residues: 651-703 <LIS>
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                                            A; Accession: A27441
                                                                                                                                                                                                                                         N; Alternate names: nonchromosomal protein C23; nucleolar
                                                                                                                                                                                                                                                                  nucleolin - Chinese hamster
:Molecule type: mRNA
:Residues: 1-713 <LAP>
                                                                                                                                                                 ;Species: Cricetulus griseus (Chinese hamster)
;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
;Accession: A27441; A24808; A24070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311-376/Domain: ribonucleoprotein repeat homology <RRM1>397-459/Domain: ribonucleoprotein repeat homology <RRM2>
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;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                    DDDDEDDDDDDEEEEEEDDSEEEVMEITPAKGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; [
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology <RRM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved
                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residue 1 as , H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences within three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                   an unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                    RESULT 5
  A; Note: host Homo sapiens (man) C; Date: 31-Dec-1992 #sequence_r C; Accession: JQ1498
                                                                     UL54 protein - human herpesvirus 2
C; Species: human herpesvirus 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 179-238 <LA3>
                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: Di
A; Residues: 1-2599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   F16M22.5
                                                                                                                                                                                                                                                                                                              l Similarity
12; Conser
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12; Conserv
                                                                                                                                                                                                                                                             9 SSQQCSSEDEDIFEETAQVSP 29
                                                                                                                                                                                                                   SSLQCPTEDEDVEEEADEVVP 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <STO>
                        #sequence_revision 31-Dec-1992 #text_change 16-Jun-2000
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, F. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wu, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wu, M.; Wu, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A96616
R;TheoLogis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown protein F16M22.5 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;308-373/Domain: ribonucleoprotein repeat homology F;394-456/Domain: ribonucleoprotein repeat homology F;486-549/Domain: ribonucleoprotein repeat homology F;572-636/Domain: ribonucleoprotein repeat homology
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A;Accession: A24070
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A; Residues: 522-541, 'G', 543-544, 'R', 546-713 <LA2>
A; Cross-references: GB:M13757; NID:g191004; PIDN:AAA36961.1;
R; Lapeyre, B.; Calzergues-Ferrer, M.; Bouche, G.; Amalric, F.
Nucleic Acids Res. 13, 5805-5816, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: nucleolin; ribonucleoprotein repeat homolog: C;Keywords: DNA binding; nucleus; phosphoprotein
                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005173; NID:g11055836; PIDN:AAG28304.1; GSPDB:GN00141
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         Conservative
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                                             28.2%;
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                                             Score 61; DB
Pred. No. 49;
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change 31-Mar-2001
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    6;
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                                                                                           Length 2599
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         Indels
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Maiti, R.;
Gaps
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(strain HG52)

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R; Kankin, C.T.; Cutright, M.T.; Makaroff, C.A.
Curr. Genet. 29, 564-571, 1996
A;Title: Characterization of the radish mitochondrial nad3/rps12 locus: analysis of recd A;Reference number: S70000; MUID:96269916; PMID:8662196
A;Accession: S70004
A;Accession: S70004
                                                                                                                                                                                                                                                                               hypothetical protein 206 - radish mitochondrion C;Species: mitochondrion Raphanus sativus (radish) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 C;Accession: S70004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: $66929
A;Accession: $66940
A;Molernia ****
                  A;Genome: mitochondrion C;Keywords: mitochondrion
                                                          A; Note: the C; Genetics:
                                                                             A; Molecule type: DNA
A; Residues: 1-206 <RAN>
A; Cross-references: GB:U43507
A; Note: the authors translated
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A;Residues: 1-395 <BOH>
A;Cross-references: EMBL:Z74965; NID:g1420194; PID:e251976; PID:g1420195; GSPDB:GN00015
A;Experimental source: strain S288C
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                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: suppressor of G2 allele of SKP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 15R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
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A; Residues: 1-512 <MCG>
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Keywords: transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
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Pred. No. 10;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIPS:YOR057w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daignan-Fornier, B.; Dang, D.V.; Valens, M. Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      es cerevisiae)
protein YOR057w
                                                                                codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                GAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 395;
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                                                                           hypothetical protein PA3074 [imported] C:Species: Pseudomonas aeruginosa C:Date: 15-Sep-2000 #sequence_revision
  C;Accession: C83262
C;Accession: C83262
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, arman. S.: Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                        DЬ
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A;Experimental source: strain S288C
R;Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle,
submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain S288C R; Pandolfo, D.; De Antoni, A.; Lanfranchi, submitted to the Protein Sequence Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002 C;Accession: S63182; S63190; S67374; S72092 R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl,
                                                                                                                                                                                                                                                          C; Genetics
                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-767 < PAF>
                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: $72092
                                                                                                                                                                                                                                                                                                                                                                                                                     R;Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G. Yeast 12, 1071-1076, 1996
A;Title: The DNA sequence of cosmid 14-5 from chromosome A;Reference number: S72073; MUID:97051596; PMID:8896273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-767 <PAW>
A;Cross-references: EMBL:Z69381; NID:g1183970; PID:e221958; PID:g1183990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: S67374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: DNA sequence of cosmid 14-5 from chromosome A; Reference number: S67355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-767 < PAN>
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A;Residues: 1-767 <DUE>
A;Cross-references: EMBL:271500; NID:g1302244; PID:e239703; PID:g1302245; MIPS:YNL224
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A; Accession: S63182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YNL224c - yeast (Saccharomyces cerevisiae) N; Alternate names: hypothetical protein N1269
                                                                                                                                                                                     A; Note:
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                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                              A; Note: the nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic
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Best Local Similarity
Matches 13; Conserv
                                                                                             Matches
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Best Local
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e: YNL224c
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181 EDDDSQNSPSTDHSLSSNESKVEDGDLFFVDEEAQQSPDLTKIKR 225
                                                                                          20;
                                                                                                                 Similarity
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                                            EDDER - - - - STD - - - SSQQCSSEDEDIF - - EETAQVSPPRGKEKR 36
                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                         acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                           EMBL:269381; NID:g1183970; PIDN:CAA93374.1; PID:g1183990 ide sequence was submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S63188
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Pred. No. 5.2;
5; Mismatches
                                                                                                              Score 59.5;
Pred. No. 21;
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                                                                                             Mismatches
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, April 1996
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S.; Olson, M.V.

15-Sep-2000

#text\_change

31-Dec-2000 (strain PAO1)

P.; Hickey, M.J. A.; Larbig, K.;

Pseudomonas aeruginosa

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A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA3074
                                                                                                                                                                                                                                                                                                 C:Genetics: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; 566/1; 608
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-44 <RES>
A; Residues: 1-44 <RES>
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PIDN: AAA39841.1; PID: g554246
A; Cross-references: GB: M22089; NID: g200111; PID: g20111; PID: g200111; PID: g
                                                                                                                                                                                                                                                                   C;Superfamily: nucleolin; ribonucleoprotein repeat homology
C;Keywords: DNA binding; duplication; nucleus; phosphoprote
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A; Residues: 1-586 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Purification and characterization of nucleolin A; Reference number: A56240; MUID:94344117; PMID:8065340 A; Accession: A56240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 2-20, X, 22-24 <PAS>
R: Yang, T.H.; Tsai, W.H.; Lee, Y.M.; Lei, H.Y.; Lai, M.Y.; Chen,
Mol. Cell. Biol. 14, 6068-6074, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:X07699; NID:g53453; PIDN:CAA30538.1; PIR;Pasternack, M.S.; Bleier, K.J.; McInerney, T.N.
J. Biol. Chem. 266, 14703-14708, 1991
A;Title: Granzyme A binding to target cell proteins. Granzyme A;Reference number: A40769; MUID:91317840; PMID:1860869
A;Accession: A40769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Structure of the mouse nucleolin A;Reference number: A29958; MUID:88316930; A;Accession: A29958
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                                                        F;489-494/Region:
                                                                                                                                                                                     F; 311-316/Region:
F; 349-356/Region:
                                                                                                                                                                                                                                             F;310-375/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 68, 73-84, 1988
A;Title: Sequence and structure of the nucleolin promoter A;Reference number: I48118; MUID:89121496; PMID:2906027
A;Accession: I84688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Bourbon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 2-19;558-567 < YAN>
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A;Residues: 1-707 <BOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004731; GB:AE004091; NID:g9949171; PIDN:AAG06462.1; GSPDB:GN00:
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                                                                                                         ;397-402/Region:
;431-438/Region:
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                                                                                   :488-551/Domain:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Mus musculus (house mouse)
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Biol. 200, 627-638, 1988
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                                                                                                         RNA-binding RNP2 motif
                                                      ribonucleoprotein repeat RNA-binding RNP2 motif
                                                                                                                                                          RNA-binding RNP1 motif ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                     inding; duplication; nucleus; phosphoprotein; RNA binding; transcripti
ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                  RNA-binding RNP2 moti
                                RNA-binding
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33.3%;
                                RNP1 motif
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Pred. No.
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     homology
                                                                                 homology <RRM3>
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        <RRM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.S.; Yeh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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UL54 protein - human herpesvirus 1
C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_:
C;Accession: I30089
                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: human herpesvirus 1
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Feb-1997
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                                                                                                            WMBEY4
                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: varicella-zoster virus gene 4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues; 1-511 < ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rosen-Wolff, A.; Frank, S.; Raab, K.; Moyal, M.; Becker, Y.; Darai, G. Virus Res. 25, 189-199, 1992
A;Title: Determination of the coding capacity of the BamHI DNA fragment B of apathoge A;Reference number: A48560; MUID:93070559; PMID:1332274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A48560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UL54 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-182 < AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T46396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Homo sapiens (man)
C; Date: 04-Feb-2000 #sequence
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                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A48560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical
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                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics
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                                                                           human herpesvirus 1 (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human herpesvirus 1 (strain HFEM)
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                           #sequence_revision
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40.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from NCBI backbone (NCBIN:117573, NCBIP:117574)
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RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.; Mewes, H.W.; Gassenhuber, nce Database, January 2000
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Pred. No.
                                                                                                                                                                                                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58.5; D
Pred. No. 6.1;
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                           31-Dec-1989 #text_change
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22;
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                                16-Jun-2000
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1;

A;Title: The complete DNA sequence of the long unique region in the genome of herpes sime. Reference number: A30083; MUID:88274327; PMID:2839594

translation not shown

.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Peri 69, 1531-1574, 1988

A; Gene: UL54

A; Molecule type: DNA A; Residues: 1-512 <MCG>

A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32290.1;

PID:g59554; GB:D00317

A; Status: nucleic acid sequence not shown;

A; Accession: I30089

R;McGeoch, D.J.; J. Gen. Virol. 6

Virol.

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RESULT 15
S20614
                                                                                          A; Molecule type: DNA
A; Residues: 1-1738 <WOL>
A; Residues: 1-1738 <WOL>
A; Cross-references: EMBL: X61368; NID:g11550; PID:g11551
R; Wolfe, K.H.; Morden, C.W.; Ems, S.C.; Palmer, J.D.
J. Mol. Evol. 35, 304-317, 1992
                                                                                                                                                                                                                      A;Title: Small single-copy region of plastid DNA in the non-photosynthetic angiosperm on at a non-bioenergetic locus.
A;Reference number: $20614; MUID:92114084; PMID:1731088
A;Accession: $20614
                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein 1738 - beechdrops plastid C;Species: plastid Epifagus virginiana (beechdrops) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Jun-1998 C;Accession: S20614; S78401; S16720
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A;Note: the authors translated the codon ATC for residue 641 as Thr
C;Superfamily: abaA protein; TEA DNA-binding domain homology
C;Keywords: DNA binding; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 57, 859-868, 1989

Cell 57, 859-868, 1989

A;Title: Interactions of three sequentially expressed genes control temporal and spatial A:Reference number: A32434; MUID:89249350; PMID:2655931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abaA protein · Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                               A; Title: Rapid evolution of the plastid translational apparatus in a A; Reference number: S78378; MUID:93021155; PMID:1404416
                                                                                                                                                                                                                                                                                                                   R; Wolfe, K.H.; Morden, C.W.; Palmer, J.D. J. Mol. Biol. 223, 95-104, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;131-201/Domain: TEA DNA-binding domain homology
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A; Residues: 1-796 <MIR>
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R; Mirabito, P.
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Keywords: transcription regulation
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6; Mismatches
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Search completed: June 17, Job time: 6.94231 secs
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A; Residues: 1-1738 < MOW>
A; Residues: 1-1738 < MOW>
A; Cross-references: EMBL: M81884; NID: 9336917; PID: 9336940
A; Note: the nucleotide sequence was submitted to the EMBL Data Library,
                                                                                                                                                                                                  C; Keywords: plastid
                                                                                                                                                                                                                     A; Genome:
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MNT_HUMAN
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## ALIGNMENTS

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SMART; SN00360; RRW; 4. SMART; SN00360; RRW; 4. PROSITE; PS00030; RRM_RNP_1; 3. Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat; RNA-binding.	MIM; 164035; InterPro; IPROUS04; RNA_rec_mot.	Aarnus/Gnent-ZDPAGE; 1210; NEPHGE. Genew; HGNC:7667; NCL.	HSSP; P09651; 1HA1.	PIR: S04631: S04631.		or send an email to license@isb-sib.ch).	a license agreement (See h	modified and this statement is not removed. Usage by and for commercial	the European Bioinformatics Institute. There are no restrictions on its	This SWISS-PROT entry is copyright. It is produced through a collaboration - hetween the Swiss Institute of Bioinformatics and the EMBL outstation -		· !- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).	ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME ASSEMBLY.	DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLAY A	EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR	-!- FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING	nucleolin gene."; J. Biol. Chem. 265:14922-14931(1990).	tion and chromosomal localization of the human	STIVESTAVE M. MORTIGO O.W. Floming D.T. Dollard H.B. Burns A.T.	SEQUENCE FROM N.A.	[2]	"Cioning and sequencing of the numba nucleotin cDNA."; FEBS Left: 250:99-105/1989).	Srivastava M., Fleming P.J., Pollard H.B., Burns A.L.;	MEDLINE=89290043; PubMed=2737305;		I_TaxID=9606;			NCL.	Protein C23).	(Rel.	16, Creat	P19338;	

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"Sequence and structure of the nucleolin pu
characterization of a strikingly conserved
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90269607; PubMed=2347493;
Bourbon H.-M., Amalric F.;
                                                                                                                                Gene 68:73-84(1988)
                                                                                                                                                                                  SEQUENCE OF 1-44 FROM N.A. MEDLINE-89121496; PubMed-2906027;
                                                                                                                                                                                                                  "Nucleolin gene organization in rodents: highly conserved sequences within three of the 13 introns.";
Gene 88:187-196(1990).
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ween the Swiss Institute of Bioinformatics Institute.
Buropean Bioinformatics Institutions as lo
                                                                                              FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLA
                                                            SUBCELLULAR LOCATION: Nuclear; nucleolar.
SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                      ROLE
         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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EMBL; M55020; AAA41732.1;
EMBL; M22090; AAA41733.1;
MEDLINE=88312631; PubMed=3409881;
Erard M.S., Belenguer P., Caizerg
Amalric F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00076; rrm; SMART; SM00360; RRM;
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HSSP; P0965
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EMBL; M55015; AAA41732.1;
                                            an unusual
Proc. Natl.
                                                              Lapeyre B., "Nucleolin,
                                                                              SEQUENCE OF 35-713 FROM N.A., AND MEDLINE=87175501; PubMed=3470736;
                                                                                                                                  Eukaryota;
                                                                                                                                                                                               P08199;
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                             FUNCTION
                                                                                                         NCBI_TaxID=10036;
                                                                                                                          Mammalia; Eutheria;
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                                                                                                                                                                                                                                                    193 DDDDEDDDDDDEEEEEEDDSEEEVMEITPAKGKK 226
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                                                                     В.,
                                                                                                                                                                                                                                                                                                Similarity
                                             protein structure revealed by the nucleotide . Acad. Sci. U.S.A. 84:1472-1476(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                   Metazoa;
                                                                                                                                                                     (Rel. 08,
(Rel. 08,
(Rel. 41,
                                                              Bourbon H., Amalric F.;
the major nucleolar protein of
                                                                                                                                                                                                                                                                                                                                                                                                                               142
187
241
310
396
488
                                                                                                                         auratus (Golden hamster).
etazoa; Chordata; Craniata
theria; Rodentia; Sciurogn
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Phosphorylation;
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Last sequence up
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          Caizergues-Ferrer M.,
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ASP/GLU-RICH (ACID)
ASP/GLU-RICH (ACID)
RNA-BINDING (RRM)
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ARG/GLY/PHE-RICH
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           Pantaloni
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HSSP; P09651; 1HA1.
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                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ondensation by binding to histone H1.";

J. Blochem. 175:525-530(1988).

FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING FUNCATION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTECING OF GROWING EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEOLAR CHROMATIN AND PREDISONAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLA ROLE IN PRET-FRAN TRANSCRIPTION AND RIBOSOME ASSEMBLY. SUBCELLULAR LOCATION: Nuclear; nucleolar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinformatics and the EMBL OULSU European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in lifted and this statement is not removed. Usage by and for confified and this statement is not removed.
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                                     12;
                                             Similarity
             EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQ
 EDEDEEEDEEEEEEEEEEEEEPVKPAPGKRKKE 283
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73
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118
                                     Conservative
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                                     8
                                   Score 63; DB
Pred. No. 3.5;
8; Mismatches
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                   37
                                                        Length 713;
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                                    Indels
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RESULT 4
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O95071; Q9NPL3; O94970;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase EDD (EC 6.3.2-) (Hyperpl
protein homolog) (hHYD) (Progestin induced protein)
EDD OR HYD OR MIAA0896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                  Deo R.C., Sonenberg N., Burley S.K.;

"X-ray structure of the human hyperplastic discs protein: an ortholog of the C-terminal domain of poly(A) binding protein.";

Proc. Natl. Acad. Sci. U.S.A. 98:4414-4419(2001).

-i- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates (By similarity). This protein may be involved in maturation and/or post-transcriptional regulation of mRNA. May play a role in control of cell cycle progression. May have tumor suppressor function. Regulates DNA topoisomerase II binding protein (TopBP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF CYS-2768.
MEDLINE-21192643; PubMed-11287654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sutherland R.L., Watts C.K.w.;
"Identification of a human HECT family protein with
"Tannhila tumor suppressor gene hyperplastic discs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta, and Heart;
MEDLINE=99153743; PubMed=10030672;
Callaghan M.J., Russell A.J., Woollatt
                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cooperation of HECT-domain ubiquitin topoisomerase II-binding protein for U. Biol. Chem. 277:3599-3605(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila tumor suppressor gene Oncogene 17:3479-3491(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Saya H., Nakao M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21671350;
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                                                                                                                                                             for the DNA damage response.
SUBCELLULAR LOCATION: Nuclear.
TISSUE Specificity: Widely expressed. Most abundant in expressed at high levels in brain, pituitary and kidney MISCELLANEOUS: A cysteine residue is required for ubique thiolester formation.
SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIQUITIN-PROTEIN L
                                                                                                                                                DOMAIN.
                                                     SWISS-PROT entry is copyright. It is produced through a collable en the Swiss Institute of Bioinformatics and the EMBL outsi European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1671350; PubMed=11714696; Tojo M., Matsuzaki K., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain;
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DNA damage response.";
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H
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http://www.isb-sib.ch/announce/

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for commercial

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Usage

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IE63_HSV2H STANDAKU;
P28276;
O1-DEC-1992 (Rel. 24, Created)
O1-DEC-1992 (Rel. 24, Last sequence update)
O1-DEC-1992 (Rel. 40, Last annotation update)
I6-CCT-2001 (Rel. 40, Last annotation update)
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SMART; SM00119; HECTC; 1.
SMART; SM00517; POLYA; 1.
SMART; SM00396; ZnF_UBR1; 1.
PROSITE; PS50237; HECT; 1.
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MUTAGEN
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                                                    Herpes simplex virus (type 2 / strain
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140
    McGeoch
     MEDLINE=92113549; PubMed=1662697; McGeoch D.J., Cunningham C., McIn
                                           Alphaherpesvirinae;
NCBI_TaxID=10315;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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InterPro: IPR002004; PABP/HECT.
InterPro: IPR000449; UBA_domain.
InterPro: IPR003126; Znf_Nrecogn:
                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bl conjugation pathway; Ligase; NOMAIN 2393 2449 PABP-
OMAIN 2462 2799 HECT
OMAIN 1986 1997 ASP/G
OMAIN 2036 2059 PRO-R
OMAIN 2357 2366 ARG/G
OMAIN 2489 2500 ASP/G
OMAIN 2737 2757 PRO-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; AB020703; BAA74
112T; 18-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF006010;
U95000; AF
                                                                                                                                                                                                                      1 EDDERSTDS---SQQCSSEDEDIFEETAQVSPP------
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                     EDDSQSNDSSDSSSSSQSDDIEQETFMLDEPLERTTNSSHANGAAQAPRSMQWAVR 1719
                                                                                                                                                                                                                                                                                     134
229
258
374
772
780
884
1811
1811
2144
2282
27489
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; AAD01259.2;
AAF88143.1; -
                                                                                                                                                                                                                                                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF88143.1; -.
BAA74919.1; -.
                                                                                                                                                                                                                                                                                                         884
1811
2144
2282
2474
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985
1537
1681
17688
2768
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7772
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                                                                                                                                                                                                                                                                                   309348
                                                                                                                                                                                                                                                      .88;
                                                                                                                                                                                                                                                                                           UBIQUITIN (BY SIMILARITY).

C->A: LOSS OF UBIQUITIN BINDING.
S-> P (IN REF. 2).
E-> K (IN REF. 2).
S-> Y (IN REF. 2).
IG-> M (IN REF. 2).
IG-> H (IN REF. 2).
D-> H (IN REF. 2).
C-> P (IN REF. 2).
C-> P (IN REF. 2).
D-> R (IN REF. 2).
S-> P (IN REF. 2).
S-> P (IN REF. 2).
K-> R (IN REF. 2).
MISSING (IN REF. 3).
MISSING (IN REF. 3).
MISSING (IN REF. 3).
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                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                     Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-SER.
POLY-ALA.
     McIntyre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASP/GLU-RICH
PRO-RICH.
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ARG/ASP-RICH
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                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; 3D-structure
                                                                                                                                                                                                                                                                                   > N (IN REF. 2).
871300DB404FF561 CRC64;
     ດ
;
                                                                 Herpesviridae;
                                                                            HG52)
                                                                                                                                                                                                                                                      DB 1;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MIXED CHARGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ACIDIC).
     Dolan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACIDIC).
                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                               Length 2799;
                                                                                                                                                                                                                                             Indels
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Best Local S
Matches · 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L_YEAST
SGT1_YEAST
Q08446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              simplex viruses
J. Gen. Virol. 7
[2]
EMBL; U88830; AAB48841.1; -. EMBL; Z70678; CAA94542.1; -. EMBL; Z74965; CAA99250.1; -.
                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 SGT1 protein.
SGT1 OR YOR057W OR YOR29-08.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D10471; BAA01269.1; -. EMBL; Z86099; CAB06702.1; -. PIR; JQ1498; WMBEXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2.", J. Gen. Virol. 72:3057-3075(1991).
                                                                                                                                                                                                           Valens M., Bohn C., Daignan-Fornier "The sequence of a 54.7 kb fragment the presence of two tRNAs and 24 new
                                                                                                                                                                                                                                                                                                          Kitagawa K., Connelly C., Hieter P., Submitted (MAR-1997) to the EMBL/Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Early protein; Tra
SEQUENCE 512 AA;
                                                                                                                                                                                              the presence of two tRN Yeast 13:379-390(1997).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
                                                                                                                                                                                                                                                             MEDLINE=97279235; PubMed=9133743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. FUNCTION: INVOLVED IN THE DOWN-REGULATION OF VITAL IMMEDIATE-EARLY GENES AND ACTS IN COMBINATION WITH ICPO AND ICP4 AS AN ACTIVATOR OF LATE GENES (BY SIMILARITY). SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54, HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DERSTDSSQQCSSEDEDIFE-----ETAQVSPPRGKEKR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription AA; 54958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35, Created)
35, Last sequence up
35, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60.5;
Pred. No. 4
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of yeast
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                                                                                                                                                                                                             reading
                                                                              http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                            V., Bolotin-Fukuhara M.; chromosome XV reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                              frames.";
                                                                                                                              restrictions
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TRESULT RESULT OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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Best Local 9
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                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 (Rel. 34, La
1970) (Rel. 34, La
1970) (Rel. 41, La)
Hypothetical 86.9 kDa pro
YNL224C OR N1269
Saccharomyces
Eukaryoth
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97051596; Pubmed-8896273;
Pandolfo D., de Antoni A., Lanfra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53866;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0005583; SEQUENCE 395
                                                                                                                                                                                                     EMBL; Z69381; CAA93374.1; -.
EMBL; Z71500; CAA96127.1; -1.
EMBL; U20390; AAA86499.1; ALT_FRAME.
EMBL; U20390; AAA86499.1; ALT_FRAME.
SGD; S0005168; YNL224C.
InterPro; IPRO0467; G_Patch.
InterPro; IPRO0467; G_Patch.
                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Duesterhoeft A., Floeth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-5 from chromosome XIV reveals reading frames including a novel gene encoding a globin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-298 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNW4_YEAST
                                                                                                                                 Hypothetical
DOMAIN 7
                                                                                                                                                                                          Pfam; PF01585; G-patch;
                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reast 12:1071-1076(1996).
                                                                      Local
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SSEDEDIFEETAQVSPPRGKEKRQW 38
                                                                                                                                                    SM00443; G-patch; 1.
E; PS50174; G_PATCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                            _
                                                                                                                                                                                                                                                                                                non-profit institutions as long and and this statement is not removed is requires a license agreement (See lean email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                        Similarity
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                             EDDER---
EDDDSQNSPSTDHSLSSNESKVEDGDLFFVDEEAQQSPDLTKIKR
                                                                                                                   767
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                                                                                                                                   720
                                                                                                                                                protein
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AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ascomycota; Saccharomycotina;
                          -STD---SSQQCSSEDEDIF--EETAQVSPPRGKEKR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetaceae;
                                                                                                                                   767
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                                                                                                                   86949 MW;
                                                                                                                                                                                                                                                                                                                                              institutions as long as its content
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                                                                      27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
protein in URB2-SSU72 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; DB Pred. No. 4.2; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fritz C.,
                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                      Score 59.5;
Pred. No. 1
                                                                                                                                G-PATCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                   CE5650B8679BF8C0 CRC64;
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                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heuss-Neitzel D.,
                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
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1.2;
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                                                                                                                                                                                                                                                                                                                            Usage
                                                         12;
                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XIV reveals
                                                                                      Length 767;
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                                                         Indels
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 INIT_MET
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Mammalia; Eutheria;
NCBI_TaxID=10090;
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                    EMBL; X07699; CAA30538.1;
EMBL; M22089; AAA39841.1;
PIR; A29958; DNMS.
                                                                                                                                                                                                                                                                                                               or send
                                                                                                                  RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 68:73-84(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89121496;
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Rodentia;
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01-MAR-1989 (Rel. 10, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
Nucleolin (Protein C23).
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Pasternack M.S., Bleier K.J., McInerney T.N.;
Pasternack A.S., Bleier K.J., McInerney T.N.;
Pasternack A.S., Bleier K.J., McInerney T.N.;
Pasternack M.S., Bleier K.J., McInerney T.N.;
Canazyme A binding to target cell proteins. Granzyme A binds to a cleaves nucleolin in vitro.

"Granzyme A binding to target cell proteins. Granzyme A binds to a cleaves nucleolin in vitro.

"Granzyme A binding to target Cell proteins. Granzyme A binding to a cleave a binding to a cleave a cleave a binding to a cleave a binding to a cleave a cleave a binding to a cleave a binding to a cleave a binding to a cleave a cleave a binding to a cleave a cle
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"Sequence and structure of the nucleolin promoter in rodents:
characterization of a strikingly conserved CpG island.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
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email to license@isb-sib.ch)
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                                                                                                                                          MCKie J.M., Wadey R.B., Sutherland H.F., Taylor C.L., S
"Direct selection of conserved cDNAs from the Dideorge
region: isolation of a novel CDC45-like gene.";
Genome Res. 8:834-841(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat CDC45-related protein (PORC-PI-1). CDC45L OR CDC45L2.
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REPEAT
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                                                                                                                                                                                                                                       "Characterization of CDC45L: a gene in the 22q11.2 expressed during murine and human development."; Mamm. Genome 10:322-326(1999).
                                                                                                                                                                                                                                                                        Shaikh T.H., Gottlieb
Emanuel B.S., Budarf
                                                                                                                                                                                                                                                                                  MEDLINE-99160479; PubMed-10051334; Shaikh T.H., Gottlieb S., Sellinger B.,
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98325026; PubMed=9660782;
Saha P., Thome K.C., Yamaguchi R., Hou Z.-H.,
"The human homolog of Saccharomyces cerevisian
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Mammalia; Eutheria;
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                                                          SUBUNIT: ASSOCIATED WITH ORC2L.

SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS ARE FOUND ADDITION TESTIS AND TYHMUS AND IN FETAL LIVER.

ADULT TESTIS AND TYHMUS AND IN FETAL LIVER.

BUT DEVELOPMENTAL STAGE: TRANSCRIPT PEAKS AT G1-S TRANSITION, BUT TOTAL PROTEIN REMAINS CONSTANT THROGGROUT THE CELL CYCLE.

EXPRESSED IN MULTIPLE TISSUES DURING EMBRYOGENESIS, INCLUDING
                                  NEURAL CREST-DERIVED STRUCTURES.
SIMILARITY: BELONGS TO THE CDC45 FAMILY.
  SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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M REPEATS OF X-T-P-
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Q99583;
15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                               Genomics 49:275-282(1998).

-!- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE
5'-CACGTG-3' AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.
-!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX
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Pfam; PF02724; CDC45; 1.
DNA replication; Cell cycle; Nuclear protein.
CONFLICT 115 115_ I -> V (IN REF.
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                                                                                                                                                                                                                    Nigro C.L., Venesio T., Reymond A Cainarca S., Enrico F., Stack M., Ballabio A., Carrozzo R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98260677;
                                                                                                                                                                                                                                                                                             heterodimerizes with Max, binds a non-canonical E transcriptional repressor."; EMBO J. 16:2892-2906(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAX binding MNT OR ROX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                          the
                                       This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                      <del>-</del>
                                                                                                                                                                                           breast tumors.",
                                                                                                                                                                                                                                                                                                                                                           Tonlorenzi R.,
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
MEDLINE=97327566; PubMed=9184233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                       "The human ROX Gene:
                                                                                                                                                                                                                                                                                                                                                                       Meroni G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM
                                                                          SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                         ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                 renzi R., Lo Nigro C., Messali S., Zo
R., Ballabio A., Carrozzo R.;
a novel bHLHZip protein expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF053074; AAC27289.1;
AF081535; AAD08998.1;
AJ223728; CAA11530.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EDDERS-----TDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                                                                                                                                                                                                                                                                                                                                     Reymond A., Alcalay M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 37, Created)
(Rel. 37, Last sequence up
(Rel. 40, Last annotation
protein MNT (ROX protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                         PubMed=9598315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
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29.8%;
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Pred. No. 9
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                                      Bioinformatics
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                                                                                                                                                                                                                              ., Meroni G., Alberici P.,
Ledbetter D.H., Liscia D.S.,
                                                                                                                                                                                                                                                                                                                                                                      Borsani G.,
                                                  It is produced through a collaboration
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(MYC antagonist MNT)
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                                      and the
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Best Local
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P79741; O91906;
15-JUN-2002 (Rel. 41, C
15-JUN-2002 (Rel. 41, L
15-JUN-2002 (Rel. 41, L
                                                                                                                                                                                               *Rawakami K., Grosshans H., Hopkins N.;

The genomic sequence of the zebrafish pescadillo gene. The Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

I- FUNCTION: May have an essential role for embryonic control of the submitted of the submitted for embryonic control of the submitted for the
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Pfam; PF00010; HLH; 1.

SMART; SM00353; HLH; 1.

PROSITE; PS00038; HLH, 1; FALSE_NEG.

PROSITE; PS50888; HLH_2; 1.
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or send a
                                                                                                                                                                                                                                                                                                             Genes
[2]
                      This
                                                                                                                                                                                                                                                                                                                            pescadillo and dead eye, essen Genes Dev. 10:3141-3155(1996).
                                                                                                                                                                                                                                                                                                                                                                                 Allende M.L., Amsterdam Hopkins N.;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-97138157; PubMed-8985183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:7188; MNT.
                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-180 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinopterygii;
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Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pescadillo
                                                                                                                                                                                                                                                                                                                                                                  "Insertional mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; Y13440; CAA73851.1; -...
L; Y13440; CAA73851.1; -...
L; Y13441; CAA73851.1; JOINED.
JL; Y13442; CAA73851.1; JOINED.
                                                  DEVELOPMENTAL STAGE: Widely and highly expressed during the first 3 days of embryogenesis. Prominent sites of expression are the eyes and optic tectum on day 1, the fin buds, liver primordium, and gut on day 2, and the branchial arches on day 3. MISCELLANEOUS: PES mutant embryos exhibit smaller eyes, a reduced brain and visceral skeleton, shortened fins and a lack of expansion of liver and gut, and die on day 6 of development. SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y13443; CAA73851.1;
Y13444; CAA73851.1;
P25912; 1HLO.
ISFAC; T03268; -
                    SWISS-PROT entry is copyright.
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio.
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299
   Institute
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34.28;
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                                                                                                                                                                                                                                                                                                                                             in zebrafish identifies essential for embryonic
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                                                                                                                                                                                                                                                   zebrafish pescadillo gene.";
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Pred. No. 9
   of
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ght. It is produced through Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                              Kawakami K., Gaiano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9;
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MBL outstation -
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SEQUENCE FROM N.A.
MEDLINE-93070559; PubMed-1332274;
Rosen-Wolff A., Frank S., Raab K., Moyal M., Becker Y.,
Rosen-Wolff the coding capacity of the BamHI DNA !
"Determination of the coding capacity of the BamHI DNA !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. It entitles requires a license agreement (See htt or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence analysis.";
Virus Res. 25:189-199(1992).
-i- FUNCTION: INVOLVED IN TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus (type 1 / strain Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-JUN-1994 (Rel. 29, Created)
Ol-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Transcriptional regulator IE63 (VMW63) (ICP27).
                         EMBL; M90438; -; NOT PIR; A48560; A48560. Early protein; Trans
                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                        PTM: PHOSPHORYLATED.

SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 154,
HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF LATE GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENES AND ACTS
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protein;
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**Ir protein; Coiled cc
269 329
323 416
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20; Conserv
                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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A
Transcription AA; 55142 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%;
34.5%;
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regulation; DNA-binding; Phosphorylation; 7BE7A8F841A98174 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
51ED59F83DFEBF34 CRC64;
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpesviridae;
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RESULT 14
ABAA_EMENI
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AC P20945
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IE63_HSV11
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Matches 11
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                     McGeoch D.J., Dalrymple M.A., Davison A.J., McNab D., Perry L.J., Scott J.E., Taylor P., "The complete DNA sequence of the long unique herpes simplex virus type 1.", J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                         J. Gen. Virol. 69:2831-2846(1988).
-!- FUNCTION: INVOLVED IN THE DOWN-REGULATION OF VIRAL IMMEDIATE-EARLY GENES AND ACTS IN COMBINATION WITH ICPO AND ICP4 AS AN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989
15-JUN-2002
   01-FEB-1991
           P20945;
                     ABAA_EMENI
                                                                                                                                                Early protein; Tra
SEQUENCE 512 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-89036163;
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                                                                                                                                                                                                                                                                                                                                                                the long unique
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                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATED.
SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
                                                                                                                                                                                                                                                                                                                 OF LATE GENES.
                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                  I30089; WMBEY4.
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(Rel. 10, Last sequence update)
(Rel. 41, Last annotation update)
onal regulator IE63 (YMW63) (ICP27).
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                                                                                                         Conservative
                                                                                                                                               Transcription regulation; DNA-binding; AA; 55252 MW; 97DF74A2B7E63A85 CRC64;
                      STANDARD;
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17, Created)
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                                                                                                        Score 58; DB Pred. No. 9.8; 6; Mismatches
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Pred. No.
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RESULT 15
YCF1_EPIVI
ID YFF1_EPIVI
AC 000383;
DT 01-APR-1993
DT 01-APR-1993
DT 15-JUN-2002
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GN YCF1.
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Matches 12
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EMBL; J04850; AAA33286.1; PIR; A32434; A32434. TRANSFAC; T01085; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mirabito P.M., Adams T.H., Timberlake W.E.; "Interactions of three sequentially expressed genes or and spatial specificity in Aspergillus development."; Cell 57:859-868(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00554; TEA_DOMAIN; 1.
Developmental protein; Conidiation; Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activator; DNA-binding; Nuclear protein.
DNA_BIND 135 200 TEA-DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENT AND CONIDIUM MATURATION. THEY ACT TOGETHER TO REGULATE THEIR OWN EXPRESSION AND OTHER SPORULATION-SPECIFIC GENES.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 1 TEA DNA-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CONTROLS TEMPORAL AND SPATIAL SPECIFICITY DEVELOPMENT. EXPRESSION OF ABAA LEADS TO ACTIVATION WETA, CESSATION OF VEGETATIVE GROWTH, AND ACCENTUATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VACUOLIZATION. FUNCTION: BRLA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEA domain: a novel, highly conserved DNA-binding motif."; 66:11-12(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00426; TEA; 1.
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12; Conserv
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. 25, Created)
. 25, Last sequence update)
. 41, Last annotation update)
kDa protein ycfl (ORF 1738).
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ams T.H., Timberlake W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABAA & WETA ARE PIVOTAL REGULATORS OF CONIDIOPHORE CONIDIUM MATURATION. THEY ACT INDIVIDUALLY AND JLATE THEIR OWN EXPRESSION AND THAT OF NUMEROUS
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MBL outstation -
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Matches 15
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MEDLINE-92114084; PubMed-1731088;

WOLFE K.H., Morden C.W., Palmer J.D.;

Wolfe K.H., Morden C.W., Palmer J.D.;

"Small single-copy region of plastid DNA in the non-photosynthetic angiosperm Epifagus virginiana contains only two genes. Differences among dicots, monocots and bryophytes in gene organization at a non-bioenergetic locus.";

J., Mol. Biol. 223:95-104(1992).
                                                                                                                                                                                                                        EMBL; X61368; CAA43644.1; -.
EMBL; M81884; AAA65870.1; -.
PIR; S16720; S16720.
PIR; S20614, S20614.
Chloroplast; Hypothetical protein.
SEQUENCE 1738 AA; 208318 MW; 6
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-93066301; PubMed-1332054;

Wolfe K.H., Morden C.W., Palmer J.D.;

"Function and evolution of a minimal plastid genome from a nonphotosynthetic parasitic plant.";

Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).

-I- FUNCTION: NOT YET KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Orobanchaceae; Epifagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epifagus virginiana (Beechdrops). Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE YCF1 FAMILY.
                                                                            245
                                                                                                                                                l Similarity 48.4
15; Conservative
                                                                                               TDSSQQCSSEDEDIFEETAQVSPPRGKEKRQ 37
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US-09-991-187-41
US-09-993-687-41
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FILING DATE: <Unknown>
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APPLICATION NUMBER: 08/990,114
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0451
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: DOS
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OPERATION DATA:
APPLICATION NUMBER: US/09/978,242
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CLASSIFICATION: CUnknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                          PRIOR FILING DATE:
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAPPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                           FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-10-04
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                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00663
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CLONE: 128842
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Hanzel, David K.
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                                                                                                                                                                                                                                                     NUMBER: PCT/US01/0066:
                                                                                                                                                                                                                                                                                           NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                      NUMBER: PCT/US01/00668
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2000-05-26
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Pred. No. 4.9;
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RESULT 4
US-10-121-988-156
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-736-4
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US-10-151-736-4
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                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                   Sequence 156, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10151736 Publication No. US20020192160A1
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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Best Local :
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                                                                                         APPLICANT: Hosken, Nancy Ann
APPLICANT: McGowan, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/AU98/00280
PRIOR FILING DATE: 1998-04-20
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/151,736
CURRENT FILING DATE: 2002-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Callaghan, Michelle J. APPLICANT: Sutherland, Lindfield
                                                        APPLICANT:
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                 APPLICANT:
                                      APPLICANT:
                                                                           APPLICANT:
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   APPLICANT:
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l Similarity 43.8%;
14; Conservation
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                                                                                                                                                                                                                                                                                         1 EDDERSTDS--SQQCSSEDEDIFEETAQVSPP--
                                                                                                                                                                                                                                                                                                                                       l Similarity 29.8
17; Conservative
                                  McGowan, Patrick
Sleath, Paul R.
Mossman, Sally P.
Evans, Lawrence S.
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Swanson, Ryan M.
McNeill, Patricia D.
                                                                                                                                                   Application US/10121988
o. US20030068327A1
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ED IN LUNG, SIGNAL = 0.87
ED IN PLACENTA, SIGNAL = 1.1
ED IN HEART, SIGNAL = 1.1
ED IN BRAIN, SIGNAL = 1.2
ED IN ADULT LIVER, SIGNAL = 1.4
ED IN HELA, SIGNAL = 0.94
ED IN HELA, SIGNAL = 6.3
ED IN HBL100, SIGNAL = 6.3
ED IN BONE MARROW, SIGNAL = 0.74
ED IN BT474, SIGNAL = 4.1
ENAUGE SIGNAL = 4.1
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Pred. No. 2.2;
6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                           Score 62; DB
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                       Mismatches
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INVENTION: COMPOSITIONS

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Best Local Similarity
Thes 12; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 156
LENGTH: 512
TYPE: PRT
ORGANISM: HSV2
US-10-121-988-156
                                                                                                                                                                                                                                                                          US-09-992-598-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-801-574-80
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                                                                                                                                                                                                                                            Sequence 41, Application US/09992598 Patent No. US20020160384A1
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Patent No. US20020081592A1
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                          APPLICANT:
                                                          APPLICANT:
                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/121,988 CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
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APPLICANT
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               PPLICANT
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                                                                                                                                                                                                                                                                                                                                   836 ETDSKKEDSSMLLSKETEDLGEDTERAHSTLDEDLERW 873
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14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                    | EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQW 38
                                                                                                                                                                                                              Ashkenazi, Avi J.
                                                         Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.
                          Grimaldi, J. Christopher Gurney, Austin L.
                                                                                                     Gerber, Hanspeter
Napier, Mary A.
                                                                                                                      Fong,
                                                                                                                                     Ferrara, Napoleone
                                                                                                                                                     Eaton, Dan
                                                                                                                                                                 Desnoyers, Luc
                                                                                                                                                                                   Botstein, David
                                                                                                                                                                                               Baker, Kevin P.
              Kljavin,Ivar J.
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                                                                                                                      Sherman
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                                                                                                                                                                                                                                                                                                                                                                                              Score 59; DB pred. No. 23; 7; Mismatches
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/
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CURRENT FILING DATE: 2001-11-14
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FILING DATE: 1998-06-05
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RESULT 7
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DR FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/090696
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Baker, Kevin P.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                      Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Godowski, Paul J.
                                                                                                                                                                       Gurney, Austin L.
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APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24

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60/090542 60/090540 60/090535 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24

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APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952

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60/089653

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CURRENT APPLICATION NUMBER: US/09/989,293A CURRENT FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-17
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                                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C61
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
 CURRENT FILING
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APPLICATION NUMBER: 60/091626
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                         Stewart,
                                                                                                                                                                                                             Roy, Margaret Ann
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                             Fong, Sherman
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No. US20020193299A1
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DR APPLICATION NUMBER: 60/088025
DR FILING DATE: 1998-06-04
DR FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06:02
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               APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088212
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OR FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-17
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US-09-990-444-41
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Best Local S
Matches 14
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                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILLING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILLING DATE: 1997-06-16
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OR APPLICATION NUMBER: 60/091982
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OR APPLICATION NUMBER: 60/090863
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OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
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FILING DATE: 1998-06-26
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Baker, Kevin P.
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Stewart, Timothy A.
Tumas, Daniel
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Gurney, Austin L.
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Goddard, Audrey
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NUMBER: 60/065311
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29.8%; Pred. No. 15;
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730p1C69
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Gurney, Austin L.
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Stewart, Timothy A.
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US-09-990-436-41
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/0
FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/
FILING DATE: 1998-04-28
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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Stewart, Timothy
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Gerritsen, Mary E
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Ferrara, Napoleone
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REFILING DATE: 1998-07-02
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FILING DATE: 1998-00 APPLICATION NUMBER: FILING DATE: 1998-00

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APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0

APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER:

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FILING DATE: 1998-06-17
APPLICATION NOTICE: 1998-06-17

APPLICATION NUMBER: FILING DATE: 1998-0

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APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/089600 TYPE DATE: 1998-06-17

NUMBER: 60/1: 1998-06-17

60/089599

R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08824
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088858
R FILING DATE: 1998-06-11

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11 OR APPLICATION NUMBER: 60/088655
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60/088217 60/088212 60/088202 60/088167

APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: FILING DATE: 1998-06

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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

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FILING DATE: 1998-06-04

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60/088033 60/088030 60/088029 60/088028 60/088026 60/088025 60/088021 60/087827

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-03

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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INTEL OF INVENTION: Acids Encoding the Same
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FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
                                                                                                                                                                                                          APPLICATION NUMBER: 60/
FILING DATE: 1998-03-20
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25
                                FILING DATE: 1998-0 APPLICATION NUMBER:
                                                            FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
                                                                                                                                           APPLICATION NUMBER: FILING DATE: 1998-0
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                                                                                                                                                                                          APPLICATION NUMBER: 60/083322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Godowski, Paul J.
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Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumas,
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: 1998-06-02
NUMBER: 60/087827
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                                60/087759
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Pred. No. 15;
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APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23

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APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252

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                                             Score 58.5;
Pred. No. 15;
                               Mismatches
                                                                DB
                                                            9
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                                                            Length 566;
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C11 CURRENT APPLICATION NUMBER: US/09/993,687 CURRENT FILING DATE: 2002-11-14
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PRIOR FILING DATE: 1997-06-16
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR APPLICATION NUMBER: 60/075945
   FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
                                                              FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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STITING DATE: 1998-06-03
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APPLICATION NUMBER:
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FILING DATE: 1998-04-28
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                                                                                                                                                   APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02
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crewart, Timothy A.
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Kljavin, Ivar J.
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Eaton, Dan L.
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FILING DATE: 1998-06 APPLICATION NUMBER:

1998-06-04 NUMBER: 60/088029

APPLICATION NUMBER:

60/088030

PRIOR

FILING DATE: APPLICATION NUMBER:

60/088326 60/088033

FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217

APPLICATION NUMBER: 60/088202

1998-06-05 1998-06-04 1998-06-04 1998-06-04 .998-06-04

60/088167

FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06

APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734

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1998-06-05

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                                                                13;
                                                              Score 58.5; D
Pred. No. 15;
13; Mismatches
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-RRRQRREWEAR 180
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                                                                Indels
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RESULT 14 US-09-989-734-41 ; Sequence 41, Application US/09989734

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PRIOR

APPLICATION NUMBER: 60/089908

APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17

FILING DATE: 1998-06-17

FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16

FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440

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APPLICATION NUMBER:

60/089514

APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598

FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861

APPLICATION NUMBER:

60/088826

APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION FILING DATE: APPLICATION FILING DATE:

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NUMBER: 60/0: 1998-06-10 NUMBER:

60/088742

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60/088738

APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER:

1998-06-11

60/088876

60/089105

FILING DATE: 1998-06-11

PRIOR

OR APPLICATION NUMBER: 60/089948
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089952
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/090246
DR FILING DATE: 1998-06-22
DR APPLICATION NUMBER: 60/090252
DR FILING DATE: 1998-06-22
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PRIOR PRIOR

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-19

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CURRENT FILING DATE: 2001-11-19
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ITLE OF INVENTION: Acids Encoding the Same
ILE REFERENCE: P2730P1C64
OR FILING DATE: 1998-06-04

OR APPLICATION NUMBER: 60/088028

OR FILING DATE: 1998-06-04

OR APPLICATION NUMBER: 60/088029

OR FILING DATE: 1998-06-04

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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
ADDITIONTION NUMBER: 60/065186
                                                                                                              APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
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FILING DATE: 1997-06-16
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Zhang, Zemin
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Williams, P. Mickey
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art, Timothy A.
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Sequence 41, Application US/09997653 Publication No. US20030008297A1 GENERAL INFORMATION:
                 APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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OR APPLICATION NUMBER: 60/087759
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/087827
OR APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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                                                                      FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087607
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Roy, Margaret Ann
Stewart, Timothy !
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PR FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-17
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50	50	50	50	50	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	51
23.1	23.1	23.1	23.1	23.1	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	. 23.4	23.4	23.4	23.4	23.6
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US-08-468-066-5	US-08-314-503A-5	US-08-466-603-5	US-08-859-937-3	US-09-382-080-3	US-08-487-072A-54	US-08-473-089-54	US-08-477-346-54	US-08-190-802A-54	US-09-968-927-18	US-09-461-240-18	US-08-301-162-18	US-08-615-170-15	US-08-615-170-6	US-09-968-927-2	US-09-461-240-2	US-08-301-162-2	US-09-134-001C-3237
Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 3, Appli	3, 2	•	Sequence 54, Appl	-	•	•	•	-		Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 3237, Ap

## ALIGNMENTS

Sequence 28. Application US/09065383 Patent No. 6391543 Patent No. 6391543  GEMERAL INFORMATION: APPLICANT: BILLING-MEDEL, PATRICIA APPLICANT: COLEN, MAURICE APPLICANT: COLEN, MAURICE APPLICANT: COLEN, MAURICE APPLICANT: COLEN, MAURICE APPLICANT: GORDON, JULIAN APPLICANT: GORDON, JULIAN APPLICANT: HONGES, STEVEN C. APPLICANT: KRATCOLVIL, JON D. APPLICANT: KRATCOLVIL, JON D. APPLICANT: RUSSELL, JOHN C. APPLICANT: RUSSELL, JOHN C. APPLICANT: STROUPE, STEPHNN D. TITLE OF INVENTION: REAGENTS AND METHODS USEFUL TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES STREET: 100 Abbott Laboratories STREET: 100 Abbott Park STATE: IL STATE: IL STATE: IL STATE: IL COUNTRY: USA ZIP: 60064-3500 COMPOTER READABLE FORM: MEDIUM TYPE: Diskette COMPOTER READABLE FORM: MEDIUM TYPE: Diskette COMPOTER READABLE FORM: APPLICATION NUMBER: US/09/065,383 FILING DATE: 23-APR-1997 ATTORNEY/AGENT INFORMATION: RESISTRATION NUMBER: US/09/065,385 FILING DATE: 23-APR-1997 ATTORNEY/AGENT INFORMATION: RESISTRATION SUMBER: 08/842,385 FILING DATE: 23-APR-1997 ATTORNEY/AGENT INFORMATION: RESISTRATION SUMBER: 08/842,385 FILING DATE: 23-APR-1997 ATTORNEY/AGENT INFORMATION: TELEPHONE: 847/935-1729 TELECOMUNICATION INFORMATION: TELEPHONE: 847/935-1729 TELECOMUNICATION TON DATA: RESISTRATION SUMBER: 08/842,385 TELEGOMUNICATION INFORMATION: TELEPHONE: 847/935-1729 TELECOMUNICATION TON SEQUENCE CHARACTERISTICS: LENGTH: 41 annino acidés LENGTH: 41 annino acidés

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; MOLECULE TYPE: US-09-065-383-27.
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Best Local Similarity
                                   Query Match
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APPLICANT: RUSSELL,
APPLICANT: STROUPE,
APPLICANT: STROUPE,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/8 FILING DATE: 23-APR-1997 ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: si
TOPOLOGY: linear
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
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ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
METHODS USEFUL
MENTION: REAGENTS AND METHODS USEFUL
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S, STEVEN C.
, MICHAEL R.
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Score 216; DB 4;
Pred. No. 9.5e-21;
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                            Length 518;
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US-08-990-114-3
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               RESULT 4
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                                                                                                                    Matches
                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 31/-
STREET: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                         248 EDEDEEEDEEEEEEEEEEEEEEPVKPAPGKRKKE 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                  l Similarity
12; Conserv
                                                                                    1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                          714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                    650-845-4166
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                                                                                                                    Conservative
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Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bandman,
                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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                                                                                                                                29.2%;
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                                                                                                                              Score 63; DB 2;
Pred. No. 2.2;
                                                                                                                 Mismatches
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                                                                                                                 17; Indels
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Sequence 3, Application US/09241333 Patent No. 6313266

GENERAL INFORMATION:

APPLICANT:

Bandman, Olga Yue, Henry Corley, Neil C.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                    Patent No.
                                       TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOFFILE REFERENCE: 6361.US.P1
                                                                    APPLICANT:
           CURRENT APPLICATION NUMBER: US/09/303,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 128842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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LE OF INVENTION:
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6221
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APPLICATION NUMBER: 09/086,503
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                                                                              ARAUJO, Fausto
SUZUKI, Yashuhi
                                                                                                     HOWARD, Lawrence V.
PARMLEY, Stephen F.
REMINGTON, Jack S.
                                                                                                                                                                                                       MAINE, Gregory T.
HUNT, Jeffery C.
                                                                                                                                                                                                                                                                                                                                                               EDDERSTDSSOQCSSEDEDIFEETAQVSPPRGKEKRQ 37
                                                                                                                                                   TYNER, Joan D.
                                                                                                                                                                          BROJANAC, Susan
JYH-TSING SHEU, Michael
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                                                                              Yashuhiro
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Pred. No. 2.
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2.2;
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US-08-132-649-6
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US-09-086-503-55
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Best Local Similarity
"~+rhes 14; Conserv:
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US-09-303-064-55
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SEQ ID NO 55
LENCTH: 667
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                  Sequence 6, Applic Patent No. 5585462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/086,503A CURRENT FILING DATE: 1998-05-28 NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHOVAN, Linda E.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, Lawrence V.
TITLE OF INVENTION: ANTIGEN COCKTAILS AND USES THEREOF
FILE REFERENCE: 6361.US.01
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TYPE: PRT
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APPLICANT:
APPLICANT:
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
                                                                                                    COUNTRY:
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 14; Conserv
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                                                                                        94105-1493
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                                                                                                                         California
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Greenberg, Andrew S.
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SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
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                                                                                                                                                                                                                                                John J.
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Pred. No.
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Pred. No.
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 Version #1.25
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13;
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                                                             ; MOLECULE TYPE: protein US-08-767-579-6
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                   Query Match
Best Local
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 Matches
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                                                                                                                                       TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Steur.
CITY: San Francisco
STATE: California
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APPLICATION NUMBER: US/08/132,649
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski,
REGISTRATION NUMBER: 37,
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                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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 Local Similarity
les 13; Conserv
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                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/767,579
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Kimmel, Alan R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONING OF PERILIPIN PROTEINS
                25.9%;
34.2%;
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                                                                                                                                                                                                                                                    Eugenia
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Pred. No. 10;
                Score 56; DB
Pred. No. 10;
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   Mismatches
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                             DB 3; Length 421;
 12;
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Gaps
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OTHER INFORMATION: 3688209
US-09-232-160-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILING DATE: 1999-01-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steve Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Laura Stuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: James Gilmore
                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
APPLICATION NUMBER: PCT/
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                  CLASSIFICATION:
                                                                                   FILING DATE:
                                                                                                   APPLICATION NUMBER:
                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 EDHEDQTDTEGEDTEEEEELETEENKFSEVAALPGPRG 335
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o. 6368794
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13; Conservative
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                                                                                                                                                                                                                                                   California
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LARKIN, Sarah B.

LARKIN, STEP-1 ISOFORMS AND USES THEREOF
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MAR, Janet H.
                                                                                                                                                                                                                                                                                                                                                                                                                     FARRANCE, Iain K.G.
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                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                   435
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                                 PCT/US95/01526
                                                                                               US/08/615,170
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Pred. No.
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 04-FE

04-FEB-1994

US 08/191,493

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INFORMATION FOR SEQ ID NO:
                                                                   TELEFAX: (212) 869-8864/974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 196:
                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 231
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                SEQUENCE CHARACTERISTICS: LENGTH: 180 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Local Similarity 31.8%;
es 14; Conservative
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STRANDEDNESS:
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                  amino acid
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08630915A
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                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOFFMAN, NO.
                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                     869-8864/9741
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DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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227
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Pred. No. 12;
6; Mismatches
                                                                                                                                                        1101-174
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RESULT 13
US-08-431-080-26
; Sequence 26, Application US/08431080
; Patent No. 5698686
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US-08-741-134-6
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Best Local Similarity
                                                                                                                                                               Matches
                                                                                                                                                                                 Query Match
Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 3.11
SOFTWARE: WordPerfect for Windows
CURRENT APPLICATION DATA:
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APPLICANT: Alnemri,
APPLICANT: Fernande
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-568-3100
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/007,163 FILING DATE: 01-NOV-1995
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                                                                                                                                                               Local Similarity
Nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                           DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Woodcock Washburn Kurtz Mackiewicz & No. One Liberty Place - 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                      linear
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28.2%;
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29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s-Alnemri, Teresa
IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerald
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                                                                                                                                                                 9;
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                                                                                                                                                               Score 55; DB Pred. No. 13; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB Pred. No. 5.2;
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                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/08938534 Patent No. 5916752
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                                                                                                                                                                                                                                                 APPLICANT: GOTTSCHAARS,
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomera
TOTTLE OF INVENTION: 32
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Vers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
                              SOFTWARE: Patentin ReL
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentir
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TELEFAX: (713) 789-2679
TELEX: 79-0924
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STRANDEDNESS: sin
FILING DATE:
                 APPLICATION NUMBER:
                                                                                                                                      COUNTRY: U
ZIP: 77210
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                                                                                                                                                                                    Houston
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P.O. Box 4433
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                                                                                                                                                    UNITED STATES
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS/ASCII
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26-SEP-1997
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35.7%;
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                                               Release #1.0, Version #1.30
                                                                                                                                                                                                                     White & Durkee
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               US/08/938,534
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RESULT 15
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Patent No. 6387619
GENERAL INFORMATION:
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                                                                      TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 26:
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PRIOR APPLICATION NUMBER:
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LENGTH: 226 amino acids
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TELEX: 79-092
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STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE: <Unknown>
                                                                                                      TELEFAX: (713) 789-2679
                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 3:
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/345,294
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UNITED STATES OF AMERICA ZIP: 77210
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STRANDEDNESS: single {	iny}
                     TYPE: amino acid
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713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singer, Miriam S.
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                                     226 amino acids
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Pred. No. 9
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SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-345-2944-26

QUETY MARICHES 15: CONSERVATIVE 8: Mismatches 15: CONSERVATIVE 8: Mismatches 11: Indels 8: Gaps 2:

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DB 146 DEDOSCOSDEDENEDENIDEVKUTAQ-----RKKRANAKA 181

Search completed: June 17, 2003, 12:03:38

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Perfect score:
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1 EDDERSTDSSQQCSS
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2: /SIDS2/gcgdata/g
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIE

10987654321	Result No.
216 216 216 216 216 216 69 65.5 65.5 65.5	Score
100.0 100.0 100.0 100.0 31.9 30.3 30.3 30.3	Query Match
41 518 518 1807 1982 1982 192 1585 1585 1585 1585	Length DB
19 23 22 22 23 23 23	!
AAM50810 AAW85472 AAM50809 ABG09728 ABG09731 AAX48248 AAE19559 ABG06075 ABG10815 ABG10815	ID
PS118 protein enco PS118 protein enco PS118 protein enco PS118 prostate mar Novel human diagno Novel human diagno Human prostate can Herpes simplex vir Novel human diagno Novel human diagno	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13.	12	11
57.5	58	58	58	58	58	58	58.5	58.5	58.5	58.5	58.5	. 59	59	59	60.5	60.5	60.5	. 62	62	62	62	62	62	62	62	62	62	62.5	64	64	64	64	65.5	65.5
			٠	•		26.9			27.1	27.1	27.1	27.3	27.3	27.3	28.0	28.0	28.0	28.7	28.7		•	•	-	28.7	•	٠	•	•	•	•	•	29.6	•	
108	774	512	117	117	117	117	566	566	566	517	214	1428	957	635	584	512	512	2799	268	268	268	268	268	268	268	268	268	642	707	707	707	536	1647	1598
22	23	23	22	22	22	22	22	22	21	23	22	22	22	22	19	19	15	19	23	22	22	22	22	22	22	22	22	22	22	20	16	22	22	22
ABG28838	51	AAE19558	AAM36518	AAM76408	AAM63593	ABB42701	AAB65164	AAU29051	AAY66641	AAU99324	AAB63963	AAG67399	AAU07894	ABG22101	AAW72152	AAW73139	AAR47811	AAW81867	ABG35521	AAM01498	AAM26151	AAM13753	AAM65886	AAM53508	ABB18177	ABB32686	ABB27527	ABB60513	AAB48964	AAW84052	AAR79912	AAB92836	ABG04001	ABG09655
Novel human diagno	GST-Herpes simplex	Herpes simplex vir	Peptide #10555 enc	Human bone marrow	Human brain expres	Peptide #10207 enc	Human PRO710 (UNQ3	Human PRO polypept	Membrane-bound pro	Human CD63 antigen	Human prostate can	Amino acid sequenc	Polypeptide sequen	Novel human diagno	2	strain	ם	tumour s	eptide	#180	#188	#18	Human bone marrow	ain e	#176	Peptide #192 encod	Human peptide #178	Drosophila melanog	nuc	Human V3 loop HIV		n prote	human	Novel human diagno

# ALIGNMENTS

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RESULT 1
AAM50810
  PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                          01-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                AAM50810;
                                                                                                                                                                                                                                                                                                                  AAM50810 standard; Protein; 41 AA.
                                                  (BILL/) BILLING-MEDEL P A. (COHE/) COHEN M. (COPL/) COPLPITTS T L. (FRIE/) FRIEDMAN P N.
                                                                                                      23-APR-1997;
                                                                                                                          23-APR-1998;
                                                                                                                                              27-DEC-2001.
                                                                                                                                                                  US2001055758-A1
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                     PS118 prostate marker immunogenic polypeptide
  (KRAT/)
                                (GRAN/)
                     HODG/
COPILITTS T L.
FRIEDMAN P N.
GORDON J.
GRANADOS E N.
HODGES S C.
KLASS M R.
KRATOCHVIL J D.
                                                                                                      97US-0842385
                                                                                                                          98US-0065383
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AAW85472
             PI PAN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
Billing-Medel PA, Conc..
Gordon J, Granados EN, Hr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraeptitelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies of diagnostic use. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease
                                                                                                 23-APR-1997;
                                                                                                                            23-APR-1998;
                                                                                                                                                                                                                                          EST clone; PS118; prostate tumour tissue; prostatic disease;
                                                                                                                                                                                                                                                                     PS118 protein
                                                                                                                                                                                                                                                                                                                                                           AAW85472 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than
                                                                                                                                                         29-OCT-1998
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                     25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               without the use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 43; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-187683/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROBE/) ROBERTS-RAPP L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
                                                                                                                                                                                                                                                                                                                                                                                                                                  1
                                                                     ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                  EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stroupe
                                                                                                                                                                                                                                                                       encoded by consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodges
                                                                                                 97US-0842385
                                                                                                                            98WO-US08239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acids
                                     Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cohen
es SC,
pe SD;
                                                                                                                                                                                                                                                                                                                                                           Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that of an immunogenic polypeptide 184-224 of human prostate-specific
       M, Colpitts TL, Hodges SC, Klass JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Coplpitts TL,
Klass MR, Krato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 216; DB 23; Pred. No. 8.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kratochvil JD,
                         MR,
                                        Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedman PN, Gordon J;
hvil JD, Roberts-Rapp L;
                        Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                            cancer
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RESULT 3
AAM50809
ID AAM5
XX AAM5
AC AAM5
XX AAM5
XX AAM5
XX PS11
XX PS11
XX PS11
XX PS11
XX PS11
XX PS17
XX P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                              (COPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803;10. The clones were identified from a cDNA library made from prostate timour tissue. Recombinant PS118 protein is used to detect PS118 specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
                                                                                                                                                                                                                                                                                                                                               (BILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostatitis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS118; prostate;
benign prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2002
  WPI; 2002-187683/24
                                                                                                   Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2001055758-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS118 prostate marker partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM50809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM50809 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostatic risk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New P118 nucleic acid and proteins - used for diagnosis treatment of prostatic disease, especially cancer, and \epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-610000/51.
                                                                                                                                                                               (KRAT/)
                                                                                                                                                                                                                                                   (GRAN/)
                                                                                                                                                                                                                                                                               (GORD/)
                                                                                                                                                                                                   KLAS/)
                                                                                                                                                                                                                               HODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
                                                                                                                                                                                                                  COPLPITTS T L.
) FRIEDMAN P N.
) GORDON J.
) GRANADOS E N.
) HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                KLASS M R.
KRATOCHVIL J
ROBERTS-RAPP
                                                  S EN,
                                                                                                                                                                                                                                                                                                                                                                      BILLING-MEDEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 100.0%;
Similarity 100.0%;
41; Conservative 0
                                                                                                                                                                                                                                                                                                                                                    COHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 93-94; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518 AA;
                                                Hodges
Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0842385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0065383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marker; prostate cancer; tumour; metastasis;
                                                Cohen M,
jes SC, Kl
ipe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                Ľ.
                                                                       M, Coplpitts TL,
Klass MR, Krato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 216; DB 19;
Pred. No. 1.7e-20;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostatic intraepithelial neoplasia;
                                                                       ts TL, Friedman Kratochvil JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                   PN,
                                                                       Roberts-Rapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518;
                                                                                                Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 4
ABG09728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus sequence is found at least 12 times more often in prostate than in non-prostate tissue. PSI18 polypeptides, including derivatives of the present sequence, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PSI18 polypeptides can be produced by expression of PSI18 polynucleotides in transfected host cells. The methods and reagents of the invention may provide an early means of detecting diseases of the prostate and may also provide new markers which can differentiate between the clinically important and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate disease -
                                                                                 WPI;
                                                                                                                                                                                                                                                      11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABA91651.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #9719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG09728 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a human prostate specific PS118
                                                                 N-PSDB;
                                                                                                                                              (HYSE-)
                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unimportant prostate cancers without the use of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide, as predicted ABA91651), and lackin
                                                                 2001-639362/73.
DB; AAS73915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                               쟵,
                                                                                                                                            HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                         2000US-0540217.
2000US-0649167.
                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 licted from a partial consensus cDNA sequence lacking the N-terminal region. The PS118
                                                                                                                                                                                                                                                                                                                                                                                                                             entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                             Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 216; DB 23;
Pred. No. 1.7e-20;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518;
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RESULT 5
ABG09731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques cc to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cmaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cdiagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human cc diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat fire wipe, introhypolitics and products of the diagnostic general countries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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                   New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assobiodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             food
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #9722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG09731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
                                                                                                     N-PSDB;
                                                                                                                                                                                     (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                         11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG09731 standard; Protein; 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1473
                                                                                                                                                                                                                                                                                                                                                                                                           supplement;
                                                                                                   2001-639362/73.
DB; AAS73918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; SEQ ID No 40087; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                   Liu C,
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                                                                                                                                                                                                                       2000US-0540217
2000US-0649167
                                                                                                                                                                                    INC.
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Pred. No. 7.1e-20;
Pred. No. 7.1e-20;
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                                              of mutations
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Claim 20;

SEQ

IJ

No 40090; 103pp; English.

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RESULT 6
AAY48248
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PC) primers, oligomers, and for chromosome polymerase chain reaction (PC) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                 New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for therapeutic agents
                                                Claim 22; 128; 166pp; German.
                                                                                                                                                         WPI; 1999-519628/44.
N-PSDB; AAZ33451.
                                                                                                                                                                                                                                                                                                                                                                                               DE19811193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag; EST; prostate tumor; antitumor; treatment;
gene therapy; tissue specificity human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate
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                                                                                                                                                                                                                 Specht T,
                                                                                                                                                                                                                                                  (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                       10-MAR-1998;
                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                             16-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY48248 standard; Protein; 192 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
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                                                                                                                                                                                                               Hinzmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer-associated protein 34
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This invention describes novel expressed at high level in prov

prostatic tumor tissue and

(A) that are encode gene

Sequence

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RESULT 7
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                             The invention also relates to the use of known agents, such as 2,2'dithiobisbenzamide (DIBA) and azodicarbonanide (ADA), and unknown agents for the manufacture of a medicament for the treatment of herpes virus infections. The method is useful for detecting agents for use in the treatment of herpes virus infections the method is useful for detecting agents for use in the treatment of herpes virus infections. The method is useful for detecting agents for use in the treatment of herpes virus infection. The present sequence is Herpes simplex virus type 2 (HSV2) IE63 protein homologue. HSV2 belongs to alphaherpes virus sub-family. IE63 protein is also called ICP27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products or their fragments. The products of the invention have antitumor activity. Polypeptides (1) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificitly, associated with known methods that use single (usually short) ESTs. AAY48215-Y48303 represent protein fragments
                                                                                                                                                                                              The invention relates to a method of detecting an agent for use the treatment of herpes virus infection. The method comprises for a herpes virus polypeptide/zinc complex; adding a test agent to
                                                                                                                                                                                                                                                                                                                Detecting an agent useful for treating herpes virus infection comprises determining any change in a polypeptide/zinc complex in the presence of the test agent .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE19559 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200204492-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus type 2 (HSV-2) IE63 protein homologue.
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                                                                                                                                                                                                                                                                                                          the test agent
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-226983/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2000; 2000GB-0016890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus infection; detection; therapy; IE63 protein; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EDDERSTDSSQQC 13
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13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     JВ,
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                                                                                                                                                                                                                                                                       English.
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Pred. No.
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0.29;
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RESULT 8
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Best Local 9
                                                                                                                                                    polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostice for energing cape marking identifications.
                                           diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in specification, but was obtained in electronic format directions.
                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 36434; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS70262.
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23-AUG-2000;
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 Sequence
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                              ftp.wipo.int/pub/published_pct_sequences.
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15; Conservative
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 1585
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2000US-0649167.
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naging; diagnostic; genetic disorder.
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                                             ar in the directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forensic;
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from WIPO
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Query Match

30.3%;

Score 65.5;

DΒ

22;

Length 1585;

Matches Query Match Best Local

l Similarity 17; Conserv

Conservative

6;

30.3%;

Score 65.5; DB Pred. No. 9.7; 6; Mismatches

DB 18;

22;

Indels Length 1585;

7;

Gaps

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Sequence

1585

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RESULT 9
ABG10815
                      CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (III) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC inaging of sites expressing (II). (I) and (II) are useful in medical CC inaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences of the invention.

CC Specification, but was obtained in electronic format directly from WIPO Cast first the but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide (II) sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT,
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2000US-0649167
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imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) is useful as hybridisation probes
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B 8

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41

В

1248 ENDENSLSSSSDCSENKDEEISEESDIEEKTEVKEEPELQTRREMEER 1295

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RESULT 10
ABG06618
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Best Local S
Matches 17
                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in disparents for a feature of the polypeptide and polypucleotide sequences have applications in disparents for a feature of the polypeptide and polypucleotide sequences have applications in the polypeptide and polypucleotide sequences have applications in the polypeptide and polypucleotide sequences have applications in the polypeptide and polypucleotide sequences have applications of the polypucleotide and polyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess to discrete.
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23-AUG-2000; 2000US-0649167
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                                                            Similarity
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EDDERSTDSSQQCS---
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--SEDEDIFEETAQVSPPRGKEKRQWRAR 41
                                                                                      Score
Pred.
                                                         ore 65.5; DB ed. No. 9.8; Mismatches
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g 24

1248 ENDENSLSSSSDCSENKDEEISEESDIEEKTEVKEEPELQTRREMEER 1295

1 EDDERSTDSSQQCS-----SEDEDIFEETAQVSPPRGKEKRQWRAR 41

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RESULT 11
ABG09655
ID ABG09
                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, (CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating (II) imaging of sites expressing (II). (I) and (II) are useful for treating (II) disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations creamino acid sequences. ABG00010-ABG30377 represent novel human of the course of the inventor.
   Matches
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Best Local :
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                                                                     Sequence
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23-AUG-2000;
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                                                                                                                        specification,
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                                                                                                                       The sequence data for this patent did not appear in the printed fication, but was obtained in electronic format directly from WIPO
   l Similarity
17; Conser
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2000US-0649167.
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                   30.3%;
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Score 65.5; D
Pred. No. 9.8;
6; Mismatches
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 18;
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RESULT 12
ABG04001
В
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II) The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC anino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG04001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG04001 standard; Protein;
 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-639362/73.
DB; AAS68188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                 L Similarity
17; Conser
ENDENSISSSSDCSENKDEEISEESDIEEKTEVKEEPELQTRREMEER 1344
                               EDDERSTDSSQQCS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                1647
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0540217
2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID No 34360;
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                                                                             30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103pp; English.
                                                                Score 65.5; E
Pred. No. 10;
6; Mismatches
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13

EDDEDDEDDDDDDEEDDSEEEAMETTPAKGKK

EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKE

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RESULT 13
AAB92836
                                                                                         CC the 502 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide comprises at least 15 nucleotides; or (b) a combination complementary strand of a polynucleotide which comprises a 5'-end complementary to the complementary to the complementary to a polynucleotide which comprises a 5'-end sequence complementary to a complementary to a polynucleotide which comprises a 3'-end sequence, where the complementary to a coligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence, 'where the combination of the 5'-end sequence,' a selected from those defined in the specification. The primer sets can be used in antisense therapy and compared the specification and/or diagnosis of the shormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cetetion and/or diagnosis of the abhormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH3363 to AAH38742 represent human cDNA sequences; and AAH3629 to AAH3632 can be also set in the exemplification considered to a considered the compared to a considered to a con
Query Match
Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB92836 standard; Protein; 536 AA
                                                                                                                                represent oligonucleotides, of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-off primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-2000;
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02-MAY-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HELI-) HELIX RES INST.
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  l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID 11383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama
                                                                                         536
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ
                                                                                         AA;
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                         29.6%;
35.3%;
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Score 64; DB Pred. No. 4.4; 6; Mismatches
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                                             DB 22;
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    16;
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                                             Length 536;
    Indels
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RESULT 14
AAR79912
ID AAR79
                                                                                                                                                                                                                                                                  RESULT 15
AAW84052
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Best Local :
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                       The protein is that of human nucleolin. An immunosuppressant contg. an antibody having reactivity to human nucleolin as the active component is claimed. The immunosuppressant is effective for various immune disease
                                                                                                                                                HIV receptor; V3 loop; human immunodeficiency virus; retrovirus; P95 protein; nucleolin; infection; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An immuno:suppressant contg. human nucleolin antibody against auto:immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human nucleolin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR79912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR79912 standard; Protein; 707
                     Region
                                                       Region
                                                                                                                          Homo sapiens
                                                                                                                                                                                   Human V3
                                                                                                                                                                                                          15-MAR-1999
                                                                                                                                                                                                                                                        AAW84052 standard; Protein; 707 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 9-11; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-355193/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIRI ) KIRIN BREWERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP07242566-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleolin; monoclonal antibody; immunosuppressant.
                                                                                                                                                                                                                                                                                                                                                                                                                              is very useful in industry.
                                                                                                                                                                                                                                                                                                               187 EDDEDDEDDDDDDEEDDSEEEAMETTPAKGKK 220
                                                                                                                                                                                                                                                                                                                                                          l Similarity
12; Conserv
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                                                                                                                                                                                  door
                                                                                                                                                                                                                                                                                                                                                                                                         707 AA;
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                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                  HIV receptor P95/nucleolin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94JP-0031668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94JP-0031668
                      185..209
                               /note= "Glu/Asp-rich region, useful as of HIV binding (claim 6)"
                                                        143..171
                                                                 /note= "Glu/Asp-rich region, useful as inhibitor
    of HIV binding (claim 6)"
                                                                                         Location/Qualifiers 22..44
            /note-
                                                                                                                                                                                                                                                                                                                                                                      29.6%;
"Glu/Asp-rich region, useful as inhibitor
  of HIV binding (claim 6)"
                                                                                                                                                                                                                                                                                                                                                             6,
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                Length 707
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                                           inhibitor
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Search completed: June 17, Job time : 12.8258 secs

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                                                                                                            Query Match
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                                                                                                                                                                                                                                                         AAW84055). P95 was identified as nucleolin by amino acid sequence analysis. The invention also concerns peptidic or non-peptidic molecules having the ability to alter and/or prevent the binding of the novel HIV receptor to the HIV retrovirus, and to pharmaceutical and diagnostic compositions containing such molecules. Methods are provided for screening for new active molecules, and to methods of
                                                                                                                                                                                                                                                                                                                                                AAW84052-54), that are implicated as cofactors in the process of HIV entry into cells. Genomic and cDNA sequences for these proteins are provided in AAV17142-45. The V3 loop HIV receptor proteins were isolated from human CD4+ CEM T-cell extracts using an affinity matrix containing either the pseudopeptide 5 (KpstCH2)NPR)-template assembled synthetic peptide or a synthetic V3 loop peptide (see AAW84055). P95 was identified as nucleolin by amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of the P95 (nucleolin) protein of the newly identified V3 loop HIV receptor. This novel protein complex receptor for HIV retroviruses consists of an association of proteins, named P95/nucleolin, P40/PHAPII and P30/PHAPI (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated V3 loop HIV receptor - comprises P95/nucleolin, P40/PHAPII and P30/PHAPI proteins, used to develop products for the treatment and prevention of HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-034588/03.
N-PSDB; AAV71742 AND AAV71745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997;
                                                                                                                                                  Sequence
                                                                                                                                                                                                       are HIV-resistant.
                                                                                                                                                                                                                   screening genetic defects in the expression of the V3 loop HIV receptor in individuals that survive long-term HIV infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 49(1); 267pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1998;
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                                                                                             Local
   187
                                    1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKE 34
                                                                          l Similarity
12; Conser
                                                                                                                                                                                  in gene therapy.
Callebaut C, Guichard G,
Krust B, Muller S;
                                                                                                                                                  707
                                                                          Conservative
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                                                                                         29.6%;
                                                                                                                                                                                                     Such genetically defective polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Glu/Asp-rich region, useful as inhibitor of HIV binding (claim 6)"
                                                                          Score 64; DB Pred. No. 6.1; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hovanessian A;
                                                                                                              DB 20;
                                                                            16;
                                                                                                              Length 707;
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Result
No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                  54.5
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria
100.0
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33.1
32.8
32.2
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Listing first 45 summaries
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180
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                                                                                                                                                                                                                                  sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_virus:*
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sp_mammal:*
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592
1807
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332
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16
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13
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Q9VPQ4
Q9GTV3
Q9GTV3
Q9VJ23
Q9VJ23
Q9VJ101
Q9G1101
Q9G117
GQ97T67
Q9G3J2
GQ97T67
Q9G3J2
GQ97T30
Q9G3J2
GQ97T30
                                                                                                         Q96CH9
Q9ULH6
Q9VHY1
Q9BLU9
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                                Q9cxs4 mus musculu
Q9ctv3 pleurotus o
Q9vf23 drosophila
Q9m010 arabidopsis
O15019 homo sapien
Q9f167 streptococc
                                                                                              Q96ch9 homo sapien
Q9ulh6 homo sapien
Q9vhy1 drosophila
Q9blu9 leishmania
Q9vpq4 drosophila
         Q963j2 drosophila
Q9jy30 neisseria m
O75370 homo sapien
                                                                                                                                                      Description
homo sapien
8 xenopus lae
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096CH9
ID 096C
AC 096C
AC 096C
DT 01-1
DT 01-1
DT 01-
DT 01-
DT 01-
DT 01-
RN 1
RN 1
RP 5
RP 5
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RA RL
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SO
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Best Local S
Matches 35
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                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                  TISSUE-COLON;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                        357
                                                                                                                          35;
                                                                                                                                    Similarity
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Q9VN67	Q96MX3	Q9UAN8	Q8R364	Q8T162	Q9LMC6	Q9C5J5	094871	Q8S0B1	Q96IL9	088778	Q9XX47	P91956	Q13249	002283	015025	Q9CUE8	Q9GLG4	Q8X0J7	Q9UQ35	Q9UHA8	042142	Q9UQ40	Q9UQ39	Q9SYH1	Q9M5P5	Q9VE96	Q83696	Q99Z56
Q9vn67 drosophila	. Q96mx3 homo sapien	Q9uan8 drosophila	Q8r364 mus musculu		Q91mc6 arabidopsis	Q9c5j5 arabidopsis	O94871 homo sapien	Q8s0bl oryza sativ	Q96il9 homo sapien	O88778 rattus norv	Q9xx47 caenorhabd1	P91956 lytechinus	Q13249 homo sapien	002283 caenorhabdi	-	Q9cue8 mus musculu		Q8x0j7 neurospora	homo	~	2 gal.	homo	Q9uq39 homo sapien		Q9m5p5 arabidopsis	Q.	Q83696 measles vir	Q99z56 streptococc

## ALIGNMENTS

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RESULT 1

O96CH9
ID C96CH9
ID C96CH9
ID C96CH9
ID C96CH9
ID C96CH9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 66.4 KDa protein (Fragment).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE-COLON;
RA Strausberg R.;
RA Strausberg R.;
RA Strausberg R.;
RA SUBMITTEN STRAIN (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RHEL; BC014227; AAH14227.1; .
RH SUDMITTEN STRAIN (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RHEL; BC014227; AAH14227.1; .
RH SUDMITTEN STRAIN (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RH Hypothetical protein.
FT NON TER 1
SO SEQUENCE 592 AA; 66400 MW; F4ALEB07B0DF47B5 CRC64;
Ouery Match 10.0%; Score 180; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES 35

OY 1 SFOSESSTPSTGGFSGKETPSEDDRSOSREHMGES 391

RESULT 2 *
OULH6 PRELIMINARY; PRT; 1807 AA.
AC 09ULH6 PRELIMINARY; PRT; 1807 AA.
AC 09ULH6 PRELIMINARY; PRT; 1807 AA.
DC 1-MAY-2000 (TTEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TTEMBLRel. 21, Last annotation update)
DE KIAA1244 protein (BIG3) (Fragment).
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RESULT

Q9VHY1

ID
Q9

DT
Q9

DT
Q9

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerbolos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Best Local :
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"KIAA1244 as a novel distantly recommendation of the EMBL/GenBank/DDBJ databases." subfamily of ARF GEFS."; the EMBL/GenBank/DDBJ databases. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB033070; BAA86558.1; -.

EMBL; AB033070; BAA86558.1; -.

EMBL; AF413080; AAL04174.1; -.

ThterPro; IPR000904; Sec7. 1.
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Pterygota; Ne
Ephydroidea;
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Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-MAY-2000
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35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1807
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Last sequence up
Last annotation
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Pred. No. 1.8e-16;
; Mismatches 0;
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spie B.C., Siden Kiamos I., Simpson M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Mu.D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
EMBL, AE003676; AAF54167.1;
DR EMBL, AE003676; AAF54167.1;
DR EMBL, AE003676; AAF54167.1;
DR InterPro; IPR001410: DFAN
  Q99 ID DT 011
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Best Local
"A physical map of the Leishmania me
Genome Res. 8:135-145(1998).
EMBL; AL513062; CAC24685.1; -
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SMART; SM00487; DEXDC; 1.
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InterPro; IPR001650; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SMART; SM00487; DEXDC; 1.
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01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                              Ivens A.C., Lewis S.M., Bagherzadeh
Smith D.F.;
                                                                                                                                                                                                                                                                                                      MEDLINE=98146435; PubMed=9477341;
                                                                                                                                                                                                                                                                                                                                    STRAIN-FRIEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         Barrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Possible SNF2-related helicase.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1061 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TremBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicase.
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51.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.,
                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ivens A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; [
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                    major
                                                                                                                                                                                                                                                                          Α.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quail M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
6.7;
                                                                                                                                                                                                                          Friedlin
                                                                                                                                                                                                                                                                          Zhang
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                                                                                                                                                                                                                    genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rajandream M.A.,
                                                                                                                                                                                                                                                                          Chan H.M.,
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RA Genorge R.A., Lewis S.E., Richards S., Ashburner m., Lewis S.E., Richards S., Zhang O., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., RA Brandon R.C., Kogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Kogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Baxter R.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Maria J.F., Aphays A.D., Barnadari D., Bolshakov S., RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Berkova D., Boltcham M.R., Bouck J., Brokstein P., Brottier P., Bouck J., Brotser K., Dahlke C., Davan B.P., Brottier P., Rah Merthiov G., Milshina N.V., Mobarty C., Worles S., Kulp D., Lai Z., Lang Y., Lin X., Rah Melson D.R., Milshina N.V., Mobarty C., Worles J., Moshrefi A., Mang Z.Y., Melson D.R., Welson D.R., Welson D.R., Brotter B., Brottier P., Shen H., Rah Melson D.R., Welson S., Pollard J., Moshrefi A., Welson D.R., Welson D.Y., R
SOUND THE PROPERTY OF THE PROP
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ATP-binding; Helicase.
SEQUENCE 1252 AA; 13789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celn
Amanatides P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker S.E., Holt R.A., Evans C.A P.G., Scherer S.E., Li P.W., Hoskins, Lewis S.E., Richards S., Ashburner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10731132;
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Last sequence update)
Last annotation update)
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Pred. No. 13;
4; Mismatches
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RESULT 7
Q96TV3
ID Q96T
AC Q96T
AC Q96T
DT 01-D
DT 01-M
DT 01-M
DT 10-M
DC Hypo
GN MV12
OS Pleu
OC Euka
OC Euka
OC NCBI
RN [1]
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Q9CXS4
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Carlinci P., de Bonaldo M.F.,
RA Blake J., Bult C., Fletcher C., Fujita M., Garlboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashtzaki Y., Storch
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 11
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Best Local
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                                                                                                                   Q96TV3
Q96TV3;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                  Pleurotus ostreatus (Oyster mushroom) (White-ro
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Agaricales; Pleurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; MEDLINE=21085660;
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01-JUN-2001
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                                                                                                 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
Hypothetical zinc finger pro
                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AKO14046; BAB29130.1; -
MGD; MGI:1920389; 3110013H01Rik.
SEQUENCE 252 AA; 27482 MW; FDEADB1DE2A6996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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NCBI_TaxID=10090;
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Mammalia; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                NCBI_TaxID=5322;
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                                                                                                                                                                                                                                                                              ATGGLSGGESPAQRSRSRTRAGAG
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                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-EMBRYONIC PubMed=11217851;
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Rodentia;
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Last
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                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                               6,
                                                                                                                                                                                                                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
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A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport U.B., Davies P.,
A Durbin K.D., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
A Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Wei M. -H., Ibegwam C.,
A Harris N.L., Harvey D., Heiman T.J., Wei M. -H., Ibegwam C.,
A Hashin D., Houston K.A., Howland T.J., Wei M. -H., Ibegwam C.,
A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Nelson D.R., Nelson D.L.,
A Nont S.M., Moy M., Murphy B., Murphy L., Muray D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Pisabarro
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Ephydroidea; Drosoph
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InterPro; IPR002893; Znf_MYND.
Pfam; PF01753; zf-MYND; 1.
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Reinert
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Metazoa; Arthropoda; Diptera; Brachycera; Musc
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01-OCT-2000
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Spier E., Spi
Svirskas R.,
                               O15019 PRELIMINARY; PRT; 2047 AA. 015019; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) KIAA0301 (DJ12208.4) (KIAA0301) (Fragment). KIAA0301 OR DJ12208.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01344; Kelch; 6.
Hypothetical protein.
SEQUENCE 621 AA; 6857
                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL161946; CAB82282.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Bevan M., Pohl T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical F7A7_180.
            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                   InterPro; IPR001798; Kelch.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     Lemcke K.,
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12; Conserv
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345 AA; 37638 MW;
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                                                                                                                                                                   SVEHKSSIYAVGGYDGKEYLNTAERFDPREH
                                                                                                                                                                                          SFQSESSTPSTGGFSGKETPSEDDRSQSREH 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSTPSTGGFSGKETPSEDDRSQSREHMGES 35
                                                                                                                                                                                                                                                                                                                                                                         (MAR-2000) to the
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Spradling A.C., Stapleton M., Stror
R., Tector C., Turner R., Venter E.,
                                                                                                                                                                                                                                                                                                                                                                                    Pohl T., Weizenegger T., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up)
(TrEMBLrel. 21, Last annotation)
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Chordata;
Primates;
                                                                                                                                                                                                                                                                 68579 MW;
                                                                                                                                                                                                                             31.1%;
38.7%;
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Pred. No.
                                                                                                                                                                                                                  Pred. No. 19; 
; Mismatches
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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, Strong R., Sun E.
ter E., Wang A.H.,
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edons; core eudicots; Rosid
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                                                                                                                                                                                                                                        Length 621;
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Eutheria;

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RESULT 12
Q97T67
ID Q97T6
AC Q97T6
DT 01-OC
DT 01-OC
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Q96117
ID Q9611
AC Q9611
DT Q1-DI
DT Q1-JI
DT Q1-JI
DT Q1-JI
DT Q1-JI
OS Homo
OC Eukar
OC Mamma
OX NCB1.
RN [1]
RP SEQUI
RC TISSU
RR STRA
SUBmi
DR EMBL.
DR Inter
DR FROS
DR PROS
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Best Local S
Matches 12
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Best Local S
Matches 15
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ day
EMBL; BC007506; AAH07506.1;
InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
ProDom; PD000425; TF_Fork_head; 1.
PROSITE; PS00657; FORK_HEAD_1; UNKNOWN_1.
PROSITE; PS00658; FORK_HEAD_2; UNKNOWN_1.
PROSITE; PS00658; FORK_HEAD_3; 1.
SEQUENCE 468 AA; 51534 MW; FE3B5805FE885680 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2000) to the ENEMBL; AB002299; BAA20761.1; --
EMBL; AL096678; CAB86660.1; --
Interpro; IPR002035; VWF_A.
SMART; SM00327; VWA; 1.
PROSITE; PS50334; VWFA; 1.
NON_TER 1 1
  097T67
097T67;
01-OCT-2001
01-OCT-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to checkpoint suppressor 1.
Homo sapiens (Human)
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Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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15; Conserv
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12; Conserv
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  (TrEMBLrel.
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                                                                       PRELIMINARY;
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Primates;
                                                                                                                                                                                                                                                                                                 30.8%;
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  18,
18,
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  Last
                          Created)
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Pred. No. 16;
5; Mismatches
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  sequence update)
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RESULT
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RESULT 13
Q963J2
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Best Local S
Matches 10
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                           NON_TER
                                                                                                                                                      "Exon organization of Ca2+ channel alpha13 subunit genes."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF371281; AAK54737.1; - FlyBase; FBgn0029846; Ca-alpha-1T.
                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                 Q963J2
Q963J2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae.";
Science 293:498-506(2001).
EMBL; AE007326; AAK74275.1; -.
TIGR; SP0088; -.
Hypothetical protein; Complete
SEQUENCE 89 AA; 9326 MW; 3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=TIGR4;
MEDLINE=21357209; PubMed=11463916;
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                                                                                                                                                                                                                                                                                                                              CA-ALPHA-1T OR CG4222 OR CG15899
                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Voltage-dependent calcium channel alphal3 subunit
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                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                             (Fragment)
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100
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ASSAAPSASGTSGASAPGERERDRDRD 126
                SESSTPSTGGFSGKETPSEDDRSQSRE
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656 AA;
                                                        Conservative
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                                                                  Score 55;
Pred. No.
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Pred. No.
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3D2136BE4CC51426 CRC64;
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                                                                                 Length 656;
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RESULT 15
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MEDILINE-99101527; PubMed-9886436;
Girbal Neuhauser E., Durieux J.J., Arnaud M., Dalbon P., Sebbag M.,
Vincent C., Simon M., Senshu T., Masson-Bessiere C.,
Volivet Reynaud C., Jolivet M., Serre G.;
"The epitopes targeted by the rheumatoid arthritis-associated antifilaggrin autoantibodies are posttranslationally generated on various sites of (pro)filaggrin by deimination of arginine residues.";
J. Immunol. 162:585-594(1999).
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075370;
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01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01.TOV-1098 (TrEMBLrel. 21, Last annotation update)
Epidermal filaggrin (Fragment).
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EMBL; AE002526; AAF42109.1;
TIGR; NMB1768; -.
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                                                                                                                                                                                       InterPro; IPR003303; Filaggrin. Pfam; PF03516; Filaggrin; 2. PRINTS; PR00487; FILAGGRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCBI_TaxID=491;
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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16; Conserv
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16; Conservative
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Search completed: June 17, 2003, 11:59:46
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US-08-467-992A-8

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US-09-065-383-27
Sequence 27, Application US/09065383
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## ALIGNMENTS

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APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/842,385
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.U
TELECOMMUNICATION:
TELEPHONE: 847/935-1729
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS.
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 60064-3500
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ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
MVENTION: REAGENTS AND METHODS USEFUL
TOP DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
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518 amino acids
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RESULT 2
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6391543e
US-09-065-383-27
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                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local Similarity
Matches 518; Conserv
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BILLIN
                                                                                                                                                                                                                                                                                                    tent No.
                                                                         APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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                                                    CORRESPONDENCE ADDRESS
                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                    APPLICANT:
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STATE:
         CITY: Abbott Park
                           STREET:
                                     ADDRESSEE:
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5. 6391543
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                        E: Abbott Laboratories 100 Abbott Park Road
                                                                                                                                                     HODGES, STEVEN C. KLASS, MICHAEL R. KRATOCHVIL, JON D.
                                                                                                                                                                                                                             FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                            COLPITTS, TRACEY L.
                                                                                                                                                                                                    GRANADOS,
                                                                                                                                                                                                                                                                         BILLING-MEDEL, PATRICIA
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; Pred. No. 2e-
0; Mismatches
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2e-277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.6%; Score 260; DB 4; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                              ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                  TITLE OF INVENTION: REAGENTS AND METHODS USEFUL TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 60)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                             STREET: 100 Abbott
CITY: Abbott Park
                                         COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
APPLICATION NUMBER:
                                                                                  MEDIUM TYPE:
                                                                                                                                                      STATE:
                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                   100 Abbott Park Road
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
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KLASS, MICHAEL R.
KRATOCHVIL, JON D
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                                                                 IBM Compatible
                                                                                                                                                                                                 Abbott Laboratories
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 US/09/065,383
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Length 40; Indels

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US-09-065-383-28
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SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842
APPLICATION START 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPAX: 847/938-2623
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                 COUNTRY:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GORDON, JULIAN
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                                                                                                                                                                                                                                                                                                                                                                                                                      KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                          RUSSELL, JOHN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BILLING-MEDEL, PATRICIA
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S, STEVEN C.
, MICHAEL R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%;
                                           08/842,385
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Pred. No.
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8e-16;
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Best Local Similarity 100.
Matches 40; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
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            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
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APPLICANT:
APPLICANT:
                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729
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SEQUENCE CHARACTERISTICS:
                                                                                                                                   FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 23-APR-1997
                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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                                             TELEFAX:
                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 60064-3500
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                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/065,383
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 371
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). 6391543
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RUSSELL, JOHN C.
STROUPE, STEPHEN D.
NVENTION: REAGENTS AN
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                                           847/938-2623
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BILLING-MEDEL, PATRICIA
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; Pred. No. 9.8e-16;
0; Mismatches 0;
                                                                                         6084.US.P1
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; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6391543e
US-09-065-383-29
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MOLECULE TYPE: peptide
US-08-729-416C-1
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Best Local Similarity 18.5%;
Matches 90; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PERRY, GLENN J.

REGISTRATION NUMBER: 28458
REFERENCE/DOCKET NUMBER: 7896
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,416C
FILING DATE: 11-CCT-1996
CIASTITICATION. 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acid
TYPE: amino acid
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                                                                                      177 QVKKVLFED---
                                                                                                                                                                    125 FDTSPGLKCLLKK------VSGIGGAANL-YRQSAMSFNIYFHALVCAVLTNQETITAE 176
219 ROWRARMPLLSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPF 278
                                       129 HMRSISFASGGDPDTTDYVAYVAKDPVNRRACHILECCDGLAQDVIGSIGQAFELRFKQY 188
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                                                                                                                                                                                                                                                      83 PGEEKTIQVPE------AKLAGFLRYI-SMQNLAVIFDLLLDSYRTARE 124
                                                                                                                            69 CEAVPGAKGAFKKRKPPSKMLSSILGKSNLQFAGMSISLTISTASLNLRTPDSKQIIANH 128
                                                                                                                                                                                                              9 PGDEPLPRPPRGTPHASDQVLGPGVTYVVKYLGCIEVLRSMRSLDFSTRTQITREAISRV 68
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20005-3918
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NOVEL BRAIN-SPECIFIC ADAPTER MOLECULE GENE
THEREOF, AND ANTIBODY THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7898/225948
                                                                                                                                                                                                                                                                                                Score 111; DB 3; Length 474; Pred. No. 0.0067; Indels 1
                                                                             -DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEK 218
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QY 83 PGEEKTIQVPE	Query Match 4.1%; Score 111; [Best Local Similarity 18.5%; Pred. No. 0.0 Matches 90; Conservative 71; Mismatches	OGY: li E TYPE: 6C-7	LENGTH: 594 amino TYPE: amino acid	ATION FOR SEQ ID NO	; TELEFAX: 202-822-0944 ; TELEX: 6714627 CUSH	LEPHONE: 202-	REGISTRATION NUM REFERENCE/DOCKET	GLENN J.	; FILING DATE: 11-UCT-1996 ; CLASSIFICATION: 536 CLASSIFICATION: 500	CATION NU	PatentIn Release #1. LICATION DATA:	ER: IBM PC COI	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	Y: USA 20005-3918	TATE: WAS	0	CE ADDRESS:	OF SECULARIES OF INVENTION: I	CANT: NAKAMURA, TAKESHI	; between of Application osygo/294100; Patent No. 6013767; GENERAL INFORMATION:	ULT 7 08-729-416C-7	Db 444 SHLINH 449	QY 488 SQLTCH 493	Db 397 GDFLVRKSTTNPGSFVLTGMHNGQAK	QY 432KRPRSGSTGSSLSVSVRDAEAQIQAW	Db 339 ALKNOPLGPVLSKAASVECISPVSPRAPDAKMLEELQAETWYQGEMSRKEAEG-	QY 385 EVKVEKKGEPLGPRGQDSPLLQRPQ-	Db 283 SDIYSTPEGKLHVA-PTGEAPTYVNT-QQIPPQAWPAAVSS	QY 325 GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTWAADKTISKLWTEYKKRKQQHNLSAFPK	Db 228 KMPPPGGFLDTRLKPRPHAPDTAQFAGKEQTYYQGR-	QY 279FILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLS	LOS EQUELATERADA DESMOSEDERWITTE
AKLAGFLRYI-SMQNLAVIFDLLLDSYRTARE 124     : :   ::  VKYLGCIEVLRSMRSLDFSTRTQITREAISRV 188	DB 3; Length 594; 0.0097; hes 205; Indels 120; Gaps 19;										ion #1.25					r. r. 	-	ADAPTER MOLECULE GENE Y THERETO						HLLLVDPEGTIRT-KDRVFDSI 443	KRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQPAVFPCI 487	LEELQAETWYQGEMSRKEAEGLLEKD 396	HLMDQG		MAADKTISKLMTEYKKRKQQHNLSAFPK 384	YQGRHLGDTFGEDWQQTPLRQGS 282	EDDRSQSREHMGESLSLKAGG 324	TEEEGDGSDHPYYNSIPS 227

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                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 829 amino acid
                                                                                           REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Humans
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           STRANDEDNESS:
                          TYPE: AMINO ACID
                                                                                 TELEPHONE:
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COPOLOGY:
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                                                                                                                                                                                                                                                                                                                                    Washington
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                                                                               202-508-9100
                                   amino acids
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           single
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                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                          Colorectal Cancer
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US-08-220-674-2
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                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            TITLE OF INVENTION: Gene M
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          APPLICANT:
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                                                                                       COUNTRY:
                                                                                                           STATE:
                                                                                                                          CITY:
                                                                                                                                                   ADDRESSEE:
                                                                                                                                      STREET:
          SOFTWARE:
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RY: U.S.A. 20001-4597

Washington D.C.

E: Banner, Birch 1001 G Street

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NATURALER, Kenneth W.
White, Raymond
Nakamura, Yusuke
VENTTON:

Gene Mutated

in Colorectal Cancer of

Vogelstein, Bert

ARE: PatentIn Rel

Release #1.0,

Version #1.25

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; ORGANISM:
US-07-670-611-2
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Best Local S
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721 AEFTNAIRREKKLKARVQELV 741
                                                                                                                      458 TNMVLTVLNQIQILPDQTFTALQ-------PAVFPCIS----QLTCHVTDIR 498
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                                                                               LVHIEHLKSEVEEQKEQRMRSLSSTSSGSKDKPGKECADAASPALSLAELRTTCSENELA
                                     VR--QAVREWLGRVGRVYDII 517
                                                                                                                                                                  QRLDLENAVLMQELMAMKEEMAELKAQLYLLEKEKK-
                                                                                                                                                                                                        SPL-LORP----QHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAW 457
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                                                                                                                                                                                                                                                                                                                                                                                                                       ---ALAESEQSLILGQFRAAGVGSSPGDQSGDENITQM
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                                                                                                                                                                  -ALELKLSTREAQEQAY
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RESULT 10
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US-08-220-674-2
                                                  Sequence 2, Application Patent No. 5576422
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GENERAL INFORMATION:
APPLICANT: Vogels
APPLICANT: Kinzle
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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LENGTH: 829 amino acids
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TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US (FILING DATE: 13-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                      LVHIEHLKSEVEEQKEQRMRSLSSTSSGSKDKPGKECADAASPALSLAELRTTCSENELA
                                                                                                                                                    AEFTNAIRREKKLKARVQELV 741
                                                                                                                                                                                                                                                                                     QRLDLENAVLMQELMAMKEEMAELKAQLYLLEKEKK -----ALELKLSTREAQEQAY
                                                                                                                                                                                     VR--QAVREWLGRVGRVYDII 517
                                                                                                                                                                                                                                                                                                                      SPL-LQRP---QHLMDQGQMRHSFSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAW
                                                                                                                                                                                                                                                                                                                                                      TSSTASSCDTEFTKEDEQ-RLKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETERLNSRIEHLKSQNDLLTITLE-----ECKSNAERMSMLVGKYESNATALRLALQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DDRSQSREHMGESLSLKAGG--GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMA 358
Vogelstein, Bert
Kinzler, Kenneth
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linear
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 Kenneth W
                                                                  US/08445186
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                                                                                                                                                                                                                                                      -----PAVFPCIS----QLTCHVTDIR 498
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; ORGANISM: Hom
US-08-445-186-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 07,
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kagan, Sarah A. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                 550 TSSTASSCDTEFTKEDEQ-RLKDYIQQLKNDRAAVKLTMLELESIHIDPLSYDVKPRGDS
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                                               ADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKG-----
                                                                                  LKRAHDCRKTAENAAKALLMKLDGSCGGAFAVAGCSVQP---
                                                                                                                 ----DDRSQSREHMGESLSLKAGG--GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMA
                                                                                                                                                    SEQCIEAYELLL-
                                                                                                                                                                                   HKLCMELCHNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKETPSE-
                                                                                                                                                                                                                     ETERLNSRIEHLKSQNDLLTITLE-----ECKSNAERMSMLVGKYESNATALRLALQY
                                                                                                                                                                                                                                                  DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLVKRL 245
                                                                                                                                                                                                                                                                                     EISSIGVSSSVAEHLAHSLQDCSNIQEIFQTLYSHG-----SAISESKIRE--FEV
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1001 G Street
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Nakamura, Yusu
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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19-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110; DB 1;
Pred. No. 0.022;
1; Mismatches 198
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Length 829;

Indels

130;

Gaps

398

349

---WESLSSNSHTST -EPLG----PRGQD

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RESULT 11
US-08-446-549-2
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US-08-446-549-2
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                                                                                                              Matches
                                                                                                                                           Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 829 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                             HYPOTHETICAL:
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                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah 
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                               Local
                                                                                                                                                                                                                                                                            COPOLOGY:
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 137 KVSGIGGAANLYRQSAMSF------
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                                              PSTGELSTSSSSNDIPIAKIAERVK-------LSKTRSESSSSDRPVLGS
                                                                              PSPGEEKTI----QVPEAKLAGFLRYISMQNLAVIFDLLLDSYRTAREFDTSPGLKCLLK
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1001 G Street
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                                                                                                              Conservative
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                                                                                                                                                                                             Homo sapiens
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13-MAR-1991
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18.4%;
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                                                                                                                             Score 110; DB 1; Length 829; Pred. No. 0.022;
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                                                                                                             Indels 130;
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                                                              TELEPHONE: 202-508-9100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                  SEQUENCE CHARACTERISTICS:
                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Kagan, Sarah A.
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                           NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                          APPLICATION NUMBER:
 STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        20001-4597
                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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White, Raymond
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US-08-446-550-2
                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application Patent No. 6280738 GENERAL INFORMATION:
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Best Local
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding F
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
                                                                                                                                            COUNTRY:
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1100 New York Avenue,
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Matches 103;
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TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 1098 amino acidi
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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APPLICATION NUMBER: US 6
FILING DATE: 06-SEP-1996
                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                              ADDRESSEE: TESIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
           STATE:
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                                                                                                                   HURWITZ & THIBEAULT
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                                                     Sequence 4, Application US/08470950 Patent No. 5698439
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                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 248-71 INFORMATION FOR SEQ ID NO:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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LENGTH: 2101 amino aci
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,390
FILING DATE: 06-JUN-1995
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MEDIUM TYPE: Floppy
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TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.82;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
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LENGTH: 2101 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
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REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MT
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                                   LSVSVRDAEAQIQAWTNMVLTVLNQIQILPD 473
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LTAQVRSLEAQV-AHADQQLRDLGKFQVATD
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Pred. No. 0.82;
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Gaps

1286 97

1336

251

Search completed: June 17, 2003, 12:03:36 Job time : 49.7804 secs

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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Match
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AAY48216
AAM50813
ABG09729
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AAM50809
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ABG09731
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AAM50812
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	Human protein sequ	AFP-1 (Ala 2460 Va	AFP-1. Homo sapie	Hs-UNC-53/3/GFP f	Human homologue of	ğ	3	Human shear stress		1 human	Novel human protei	1 human	1 human	1 human	l human	l human	1 human	۳,	$\sim$	1 human	l human	L human s	cancer asso	brain-s	n brain-	l human	l human	1 human	1 human	l human	=	melano		phila mela	PS118 prostate mar

## ALIGNMENTS

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RESULT 1
AAW85472
ID AAW85472
ID AAW85472
AC AAW8
XX AAW8
AC A
                                                                                                                                     WPI; 1998-610000/51.
N-PSDB; AAV82812.
                                                                                                                                                                                                                                                                          Billing-Medel PA, Cohen
Gordon J, Granados EN,
Robert-Srapp L, Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1998;
New P118 nucleic acid and proteins - used for diagnosis and treatment of prostatic disease, especially cancer, and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US08239
                                                                                                                                                                                                                                                                     A, Cohen M, Colpitts TL, ados EN, Hodges SC, Klass Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                               Friedman PN;
MR, Kratochvil JD;
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for drug

EST clone; PS118; prostate tumour tissue; prostatic disease; cancer

PS118 protein encoded by consensus sequence

AAW85472;

25-FEB-1999 (first entry)

AAW85472 standard; Protein; 518 AA.

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RESULT 2
AAM50809
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Best Local (
       PS118; prostate; marker; prostate cancer; tumour; metas benign prostatic hyperplasia; prostatic intraepithelial prostatitis; human; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is encoded by consensus PS118 sequence derived from overlapping EST (expressed sequence tag) clones AAV82803-10. The clones were identified from a CDNA library made from prostate tumour tissue. Recombinant PS118 protein is used to detect PS118-specific antibodies, to raise antibodies for detection of PS118 antigens, to screen for specific binding agents (potential therapeutics, and to isolate specific antibodies from serum. Detection of PS118 protein or nucleic acid, which are prostate related, and altered or elevated in prostatic disease, is used for detection, diagnosis, staging, monitoring and prognosis of prostatic disease, particularly cancer, and to identify subjects at
                                                                                                                                                             AAM50809
                                                                                                     01-MAY-2002
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18; Conservative
                                                                                                                                                                                                                                    KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
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                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                              FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW
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                                                                                                                                                                                                                                                                                              FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 AA;
                                                                       marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93-94; 117pp;
                                                                                                                                                             Protein;
                                                                                                  entry)
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                                                                    partial sequence.
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Pred. No. 1e-253;
; Mismatches 0;
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                          neoplasia;
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В δõ

121 181

TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK 180

120

60

VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW

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                                                                                                                                                                                             The present sequence is that of a human prostate-specific PS118

C polypeptide, as predicted from a partial consensus CDNA sequence

C (see ABA91651), and lacking the N-terminal region. The PS118

C consensus sequence is found at least 12 times more often in

prostate than in non-prostate tissue. PS118 polypeptides,

including derivatives of the present sequence, polynucleotides,

c antibodies, agonists and inhibitors are useful for detecting,

diagnosing, staging, monitoring, prognosticating, preventing and

treating (including by genetic immunisation), or determining the

prostate, such as benign prostatic hyperplasia, prostatitis,

prostate, such as benign prostatic hyperplasia, prostatitis,

prostate intraepithelial neophasia, prostate cancer, tumours and

metastases. The PS118 polypeptides can be produced by expression

of PS118 polynucleotides in transfected host cells. The methods

and reagents of the invention may provide an early means of

detecting diseases of the prostate and may also provide new markers

which can differentiate between the clinically important and

unimportant prostate cancers without the use of surgery.
                                                                                                                Best Loc
Matches
                                                                                                                                            Query Match
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting presence of target PS118 polynucleotide in test sample, useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating or determining predisposition to prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granados
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DB; ABA91651.
                                                                                                                al Similarity
518; Conserv
 61
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) GORDON J.
) GRANADOS E N.
) HODGES S C.
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) KRATOCHVIL J
) ROBERTS-RAPP
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              SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR 120
                                                                       RIRAMAQQVEMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSYSFREIVVSLL
SHQVLLQNLYDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQNLAVIFDLLLDSYR
                                                        RIRAMAQQVFMLDTQCSPKTPNNFDHAQSCQLIIELPPDEKPNGHTKKSVSFREIVVSLL
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ilarity 100.0%;
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rpe SD;
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                                                                                                           Score 2698; DB 23;
Pred. No. 1e-253;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess biodiversity -
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23-AUG-2000;
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DB; AAS73915.
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disorders involving aberrant protein expression or biology The polypeptide and polynucleotide sequences have applicat diagnostics, forensics, gene mapping, identification of must responsible for genetic disorders or other traits to assess and to produce other types of data and products dependent amino acid sequences. ABG00010-ABG30377 represent novel humalization acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIF at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                      VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW
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                                                                                              FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
                                                                                                                                               KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV
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ABG09731 standard; Protein; 1982 AA.

ABG09731;

13-FEB-2002 (first entry)

Novel human diagnostic protein #9722.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mittations.
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23-AUG-2000;
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DB; AAS73918.
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KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS
                                                                {\tt LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE}
                                                                                                                                                                                             LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE
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99.2%;
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Pred. No. 4.2e-242;
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RESULT 5
AAY48248
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     Query Match
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Matches 192
                                                                                                        therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAY48215-Y48303 represent protein fragments encoded by the expressed sequence tags described in the method of the
                                                                                                                                                                                                                                                   This invention describes novel nucleic acid sequences (A) that are expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid expressed at high level in prostatic tumor tissue encoded polypeptides, useful for treating cancer and screening for therapeutic agents \,
                                                                                                                                                                                                                                                                                                                                                     Claim 22; 128; 166pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-519628/44.
N-PSDB; AAZ33451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (META-) METAGEN GES GENOMFORSCHUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tag; EST; prostate tumor; antitumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cancer-associated protein 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY48248 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999
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                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ
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                                                                     192
     Conservative
                                                                   ÅA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue specificity human
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                    36.4%;
100.0%;
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 0; Mismatches
                  Score 982;
Pred. No.
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                DB 20;
3.7e-87;
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                                Length 192;
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment;
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RESULT 6
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             S
                                                 Query Match
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Matches 180
                                                                                                                                                                         expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAY48215-Y48303 represent protein fragments encoded by the expressed sequence tags described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22; 112-113; 166pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid expressed at hig encoded polypeptides, useful for therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate
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                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Specht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (META-) METAGEN GES GENOMFORSCHUNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed sequence tag; EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
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                                                     180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                     Similarity
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               MLDTQCSPKTPNNFDHAQSCQLITELPPDEKPNGHTKKSVSFREIVVSLLSHQVLLQNLY
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                                                                                                                          180
                                                     Conservative
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                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                   0;
                                                                     Score 920;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate tumor; antitumor; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    high level in
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                                                 3.7e-81;
thes 0;
                                                                                        DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostatic tumor tissue ancer and screening for
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                                                                                      Length 180;
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                                                   0;
                                                   Gaps
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RESULT 7
AAM50813
The present sequence is that of an immunogenic polypeptide comprising amino acids 393-441 of human prostate-specific PS118 polypeptide (see AAM50809). A PS118 consensus sequence (see ABA9151) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the prostate, such as benign prostatic interaptibelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Billing-Medel PA, Co
Granados EN, Hodges
Russell JC, Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS118; prostate; marker; prostate cancer; tumour; benign prostatic hyperplasia; prostatic intraepiti prostatitis; human; diagnosis; therapy; vaccine;
                                                                                                                                                                                                                                                                                                       Claim 17; Page 44; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                        Detecting presence of target PS118 polynucleotide in tes useful for detecting, diagnosing, staging, monitoring, p preventing or treating or determining predisposition to disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-187683/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRATOCHVIL J D.
ROBERTS-RAPP L.
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HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLASS M R.
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jes SC,
ipe SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coplpitts TL, Friedman
ass MR, Kratochvil JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon J;
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        CC polymerase chain reaction (PCR) primers, olligomers, and for chromosome C and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical climaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG3037 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 40088; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #9720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                     polypeptide (II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     supplement;
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sequences
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maging; diagnostic;
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Pred. No. 1e-17;
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 of the invention
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                                                                                                                                                                                                                                                                                   polynucleotide (I) and
                                                                                                                                                                                                                                                                   useful as hybridisation probes
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genetic disorder.
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Best Local S
Matches 49
       polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the
                                                                                             comprising amino acids
                                                                                                                                  Claim 17; Page 43;
                                                                                                                                                                     preventing
                                                                                                                                                                                              Detecting
                                                                                                                                                                                                                       WPI; 2002-187683/24.
                                                                                                                                                                                                                                                                                                                                                                                             (BILL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS118; prostate; marker; prostate cancer; tumour; metastasis; benign prostatic hyperplasia; prostatic intraepithelial neoplasia; prostatitis; human; diagnosis; therapy; vaccine; immunogen.
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                                                                                                           The present sequence is that of an immunogenic polypeptide
                                                                                                                                                                                                                                               Russell
                                                                                                                                                                                                                                                           Granados
                                                                                                                                                                                                                                                                      Billing-Medel PA,
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                                                                                                                                                                                                                                               JC,
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HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                  FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                                                                                                             COHEN
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                                                                                                                                                                                                                                                                                                                                                            GORDON J
                                                                                                                                                                                                                                                                                                                                                                                   COPLPITTS
                                                                                                                                                                                                                                                                                                                                                                                                          BILLING-MEDEL P
                                                                                                                                                                                                                                                                                                          KRATOCHVIL J
                                                                                                                                                                                                                                                                                                                      KLASS M R.
                                                                                                                                                                                                                                                         EN,
                                                                                                                                                                                   presence of target PS118 polynucleotide in test sample r detecting, diagnosing, staging, monitoring, prognosti
                                                                                                                                                                       or treating
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                                                                                                                                 57pp;
                                                                                                                                                                                                                                              Cohen M, Coplpitts TL, Friedman es SC, Klass MR, Kratochvil JD, pe SD;
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98.0%;
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                                                                                             184-224 of human prostate-specific PS118
                                                                                                                                  English.
                                                                                                                                                                       determining
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No. 3.3e-17;
                                                                                                                                                                       predisposition
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                                                                                                                                                                       to prostate
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                                                                                                                                                                                   prognosticating,
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                                                                                                                                                                                                                                                                       Gordon J;
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Best Local
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The present sequence is that of an immunogenic polypeptide comprising amino acids 332-371 of human prostate-specific PS118 polypeptide (see AAM50809). A PS118 consensus sequence (see ABA91651) is found at least 12 times more often in prostate than
                                                                                                          Claim 17;
                                                                                                                                                           Detecting presence of target PS118 polynucleotide in useful for detecting, diagnosing, staging, monitoring preventing or treating or determining predisposition disease.
                                                                                                                                                                                                                                                             WPI; 2002-187683/24.
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(FRIE/)
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benign prostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KLAS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate marker
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                                                                                                                                                                                                                                                                                            JC,
                                                                                                                                                                                                                                                                                                                                                                                    KLASS M.R.
KRATOCHVIL J
ROBERTS-RAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BILLING-MEDEL P
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HODGES S C.
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llarity 100.0%;
Conservative (
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Stroupe
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                                                                                                                                                                                                                                                                                                     Cohen
es SC,
pe SD;
                                                                                                        57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                                                                                        ging, monitoring, predisposition to
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. 1.5e-13;
ches 0;
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Roberts-Rapp
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prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in non-prostate tissue. PS118 polypeptides, polynucleotides, antibodies, agonists and inhibitors are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing and treating (including by genetic immunisation), or determining the predisposition of an individual to, diseases and conditions of the prostate, such as benign prostatic hyperplasia, prostatitis, prostatic intraepithelial neoplasia, prostate cancer, tumours and metastases. The PS118 polypeptides can be produced by expression of PS118 polynucleotides in transfected host cells, and immunogenic peptides are useful for raising PS118-specific antibodies of diagnostic use. The methods and reagents of the prostate and may also provide new markers which can differentiate between the clinically important and unimportant prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                  Detecting presence of target PS118 pouseful for detecting, diagnosing, starpreventing or treating or determining
                                                                                                                                                                                                                                                                                                                                                                        PS118; prostate;
benign prostatic
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(COPL/)
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les 40; Conser
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) FRIEDMAN P N.
) GORDON J.
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                                                                              JC,
                                                                                                                              KLASS M R.
KRATOCHVIL J
ROBERTS-RAPP
                                                                                                                                                             GRANADOS E N.
HODGES S C.
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                                                                                                                                                                                                                              BILLING - MEDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                               marker; prostate cancer; tumour; metastasis;
hyperplasia; prostatic intraepithelial qeoplasia;
an; diagnosis; therapy; vaccine; immunogén.
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les SC,
lpe SD;
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                                                                                              Coplpitts TL, Frie
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Pred. No.
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                  8 polynucleotide in the staging, monitoring, ning predisposition to
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g, prognosticating,
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     capable
useful i
                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                           Disclosure;
                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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2000US-0614150.
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Pred. No. 3.8e-1
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RESULT 13
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila.;The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insecticides, therapeutics and pharmaceutical drugs. The inventicities genomic DNA sequences (ABL16176-ABL30511), expressed Escuences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                             Disclosure;
                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                    genes
                                                                                                              New isolated nucleic
                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                 (PEKE )
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11-JUL-2000;
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DB; ABL08415.
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Pred. No. 3.6
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 The
                    Disclosure;
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11-JUL-2000;
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                                                                                                                                                                                                                                                      Drosophila melanogaster
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                                                                                                                                                                                                                                                                                     Drosophila; developmental biology;
                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SEDEKERKRKKKSKRSRKESASEDEWVEAPPPLAADNVTKKEPPQRDDW-----
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RESULT 15
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Matches 105
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                                                                                                                            Novel human protein (NHP) #17.
                                                                                                                                                                                                              AAE09851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
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                                                                                        Human; novel cerebellin;
                                                                                                                                                           29-NOV-2001
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105; Conservative
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                                                                                     novel human protein;
                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVALSEMSDNRAQSIQSLHSVLETPTPDTTP-----SFDELQQRLEASNRNMQHLHD
                                                                                                                                                                                                                                                                                                                                                           KEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGP--ELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                       LNDV----TSELRAEAASLQKE-----
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                                                                                                                                                                                                                                                                                                      SLSVSVRDAEAQIQAWTN 459
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                                                                                                    protein; NHP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encode or act as NHP antisense molecules, or may be used as part of ribozyme and/or triple helix sequences. Addressable arrays comprising the NHP can be used to identify and characterise the tissue expression of a gene. The use of addressable arrays comprising the NHP provide detailed information about transcriptional changes involved in specific pathway, potentially leading to the identification of novel components or gene functions that manifest themselves as novel phenotypes. The NHPs are also useful for identifying mutations associated with a particular disease. The present sequence is a NHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polynucleotides encoding proteins that share sequence similarity with mammalian membrane proteins, useful as hybridization probes for screening libraries and assessing gene expression patterns
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N-PSDB; AAD16957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199
356 KQETPKLWPVQLQKEQDPKKQTPKSWTPSMQSEQNTTKSWTTPMCEEQDSKQPETPKSWE
                                                                                    298 GKETP-----SEDDRSQSREHMGESL-SIKAGGGDLILPPSPKVEKKDPSRKKEWW 347
                                                                                                                                                                                                                                                        243 KRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGF----S
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Search completed: June 17, Job time: 151.408 secs 2003, 11:55:55

Title: Perfect score: Sequence:

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GenCore (c) 1993

Scoring

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             Interpro; IPRO00330; SNP2_N.

Pfam; PF00176; SNP2_N; 1.

Pfam; PF00271; helicase_C; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00490; HELICC; 1.

SMART; SM00490; Helicase; ATP-binding.

Nuclear protein; Helicase; ATP-binding.

NP_BIND 465 472

NP_BIND 603 606

SEQUENCE 1061 AA; 118189 MW; E82AA64254342BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
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Probable helicase)
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Peterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDS_DROME P34739;
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between, the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                         CONCEPTUAL TRANSLATION.
MEDLINE-93181281; PubMed-8382805;
Bork P., Koonin E.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in lodestar, a Drosophila gene
triphosphate-binding protein.";
Genes Dev. 5:1786-1799(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Girdham C.G., Glover D.M.;

"Chromosome tangling and breakage at anaphase result from mutations"

"Chromosome tangling and breakage at anaphase result from mutations

"Chromosome tangling and breakage at anaphase result from mutations

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MEDLINE=92009170; Pubmed=1916263;
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FlyBase; FBgn0002542; lds.
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                                                                                                                                                                                                            InterPro; IPR001410;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor (EC 2.3.1:12) (E2) (PDC-E2)
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Pfam; PF00364; biotin_lipoyl; 2.
Pfam; PF02817; e3_binding; 1.
ProDom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00189; LIPOYL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U06634; AAA
HSSP; P10515; 1FY
DictyDb; DD05070;
                                                                                                                                                                                           PROSITE; PS00189; LIPOYL; \overline{2}.
Glycolysis; Transferase; Acyltransferase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mycetozoa;
NCBI_TaxID=44689;
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Eukaryota; Mycetozoa; Dictyosteliida;
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                                                                                                                                                                                                                                                                                                                           InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR000089; Biotin_lipoyi.
InterPro; IPR004167; E3_bhiding.
InterPro; IPR003016; Lipoyl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: 20 TO 30 ALPHA(2)-BETA(2) TETRAMERS OF E1 OF E3 + 60 COPIES OF E2.
SUBCELLULAR LOCATION: Mitochondrial matrix.
SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE SIMILARITY: CONTAINS 2 LIPOYL-BINDING DOMAINS.
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                    COMPONENT OF PYRUV COMPLEX.
LIPOYL BINDING 1.
LIPOYL BINDING 2.
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30-MAY-2000 (Rel. 3
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MEDLINE-97299653; PubMed-9154802;

Pati D., Keller C., Groudine M., Plon S.E.;

Pati D., Keller of a MEC1-independent checkpoint

"Reconstitution of a MEC1-independent checkpoint

expression of a novel human fork head cDNA.";

Mol. Cell. Biol. 17:3037-3046(1997).
                                      Transcription regulation; DNA-binding; DNA_BIND 113 204 FORK-HEAD SEQUENCE 490 AA; 53834 MW; EE07975;
                                                                                                       PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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Mammalia; Eutheria;
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PRODOM; PD000425; TF_Fork_head;
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                                                                                  Nuclear protein
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YW04_SCHPO
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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Oliver K., Mutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Nature 415:871-880(2002).

"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
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15-JUN-2002 (Rel. 41, Last annotation updat
Hypothetical protein C543.04 in chromosome
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16-OCT-2001 (Rel. 40,
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scomycota; Schizosaccharomycetes;
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                                                                                                  Score 55;
Pred. No.
                                                         Pred. No. 9.6;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mont S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson K.R., Nelson K.N., Nixon K., Nusskern D.R., Pacleb J.M., Nelson K.R., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Water B., Water B., Water B., Wang X., Water B., Water B., Water B., Water B., Water B., Water B., Wang X., Water B., Wat
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Doult L.B., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Falst M., Folker R., Markey B., Walley B., Bellin M.-H., Ibegwam C.,
Falst M., Falst R., Folker R., Box R., Folker R.,
Falst M., Falst R., Folker R., Folker R.,
Falst M., Folker R., Folker R., Folker R.,
Falst M., Falst R., Howland T.J., Wei M.-H., Ibegwam C.,
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                              FlyBase;
                                                                EMBL;
                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                            modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                    003603; AAF52038.1;
FBgn0037316; CG2669
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1 (Rel. 40, Last annotation update)
of son gene protein homolog
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P.G., Scherer S.E., Li P.W.,
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i P.W., Hoskins R.A., Galle
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В. F.,
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RESULT 6
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        EMBL; Y10262; CA
EMBL; U81602; AA
EMBL; AJ007991;
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SEQUENCE OF 413-531 FROM N.A.
MEDLINE-99105912; PubMed-9887327;
Borsani G., DeGrandi A., Ballabio A
Banfi S., Gattuso C., Mariani M., [
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15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                   use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Vincent C., Weil D., Cruaud C., Sahly I.,
Bitner-Gindzicz M., Francis M., Lacombe
Charachon R., Boven K., Bedbeder P., van
Weissenbach J., Petit C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYA3
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Genew; HGNC:3521;
                                                                                                   the
                                                                                                                                                                                          Hum.
                                                                                                                                                                                                                                                                                         "Cloning and characterization of two Drosophila eyes absent gene."; Genome Res. 7:128-141(1997).
                                                                                                                                                                                                                                                                                                                                      Genin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo;
MEDLINE=97172972;
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                                                                                                                                                                                                 "EYA4,
                                                                                                                                                                                                                                                                                                                                    Zimmerman J.E., Bui Q.T., Steingrimsson Genin A., Spinner N.B., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                               lanson I.;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97202104; PubMed-9049631;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Weissenbach J., Petit C.;
"A human homologue of the Drosophila eyes absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                            A4, a novel vertebrate gene related to Dro Mol. Genet. 8:11-23(1999).
FUNCTION: MAY BE INVOLVED IN DEVELOPMENT ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOW PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE EYA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        absent
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       ; CAA71311.1; -.; AAB42066.1; -.
91; CAA07814.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9020840,
                                                                                                                                                                                                                                                                                                                                                                                (ISOFORM 2).
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Vi
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                                                                                                                                                                                                                                   A., Bulfone A., Bernard
Dixon M., Donnai D., Me
                                                                                                                                                                                                                                                                                                                                                                                                                            and identifies
                                                                                                                                                                                                                          Brown
                                                                                                                                                                                                                                                                                                                vertebrate homologs of the
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                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                     Jenkins
                                                                                 There are no restrictions ong as its content is in
                                                                                                                                                                   (SHOWN
                                                                                                                                                                                                                       Α.,
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Leibovici M.,
D., Vigneron J.,
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ins N.A.,
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AC P16054
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Best Local S
Matches 15
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          Oncogene
                                                                                                                                                                                                                                                                    P16054;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein kinase C, epsilon type (EC 2.7.1.-) (
                   Mushinski J.F.;
"The catalytic domain of PKC-epsilon, in recipro epsilon chimeras, is responsible for conferring NIH3T3 cells, whereas both regulatory and cataly PKC-epsilon contribute to in vitro transformatio Oncogene 16:53-60(1998).
                                                                                     MEDLINE-98127436; PubMed-9467942; Wand O.J., Acs P., Goodnight J.,
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89137541; PubMed-2917656;
Schaap D., Parker P.J., Bristol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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Mammalia; Eutheria;
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SEQUENCE FROM N.A
                                                                                                             TISSUE=Brain;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                      PKC-epsilon: a
                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                      KPCE_MOUSE
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                                                                                                                                                                   "Unique
                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                             236 TYQSEKPSVMAPAPAAQKLSSGDPSTSPSLSQTTPSKDTDDQSRKNM
                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
15; Conser
                                                                                                                                         D., Parker P.J., Bristol A., Kriz R., substrate specificity and regulatory ilon: a rationale for diversity."; tt. 243:351-357(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                  SFQSE---
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283
290
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Rodentia;
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                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EBE1F6435295CAC5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                      Blumberg P.M.,
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                              ory and catalytic transformation.";
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                                                                                                                                                                             Knopf J.;
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                                                                                      Mischak
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RESULT 8
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Best Local S
Matches 12
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PRODOM; PRO00001; EUK_PKINASE; 1.
PRODOM; PRO000001; EUK_PKINASE; 1.
SMART; SM00109; C1; 1.
SMART; SM00209; C2; 1.
SMART; SM00230; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS500118; PROTEIN_KINASE_ST; 1.
PROSITE; PS500118; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR0007219; Euk_pkinase.
InterPro; IPR000719; Euk_hinase_C.
InterPro; IPR0002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00133; pkinase_C; 1.
                                                                                                                                                                                                      NP_BIND
BINDING
ACT_SITE
MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF028009; AAB84189.1; -. EMBL; AF325507; AAG53692.1; -. PIR; S02270; KIMSCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wheeler D.L.;
Submitted (DEC-2000)
 KPCE_RAT
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                        Repeat; ATP-binding; Tra
Serine/threonine-protein
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MGD; MGI:97599; Prkce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-BEPENDENT,
SERINE- AND THEGONINE-SPECIFIC ENZYME.
SERINE- AND THEGONINE-SPECIFIC ENZYME.
FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES A
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
BINDING DOMAINS.
SIMILARITY: CONTAINS 1 C2 DOMAIN.
SIMILARITY: CONTAINS 1 C2 DOMAIN.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                         327
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                                                                                                                                              Similarity
                                                                                                   SESSTPSTGGFSGKETPSEDDRSOS
                                                                         AESPQPASG----NSPSEDDRSKS
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243
408
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 STANDARD;
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                                                                                                                                              29.78;
                                                                                                                                                                                           X
X
                                                                                                                              Score 53.5; I
Pred. No. 20;
5; Mismatches
                                                                                                                                                                                                                                   PHORBOL-ESTER AND DAG E PHORBOL-ESTER AND DAG E PHORBOL STEEL KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                         PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
7AEBBBCC10C99F57 CRC64;
   PRT;
                                                                                                                                              53.5;
No. 20;
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R PRODUCT, ENGUAGE 1.

RR SMART; SMO0109; C1; 2.

RR SMART; SM00139; C2; 1.

RR SMART; SM00133; S_TK_X; 1.

RR SMART; SM00133; S_TK_X; 1.

RR SMART; SM00133; S_TK_X; 1.

RR SMART; SM00220; S_TKC; 1.

RP PROSITE; PSS00047; DAG_PE_BIND_DOM_1; 2.

RR PROSITE; PSS0010; DAG_PE_BIND_DOM_2; 2.

RR PROSITE; PSS00107; PROTEIN_KIMASE_DOM; 1.

RR PROSITE; PSS00107; PROTEIN_KIMASE_DOM; 1.

RR PROSITE; PSS00107; PROTEIN_KIMASE_DOM; 1.

RR PROSITE; PSS00107; PROTEIN_KIMASE_ST; 1.

RR PROSITE; PSS00108; PROTEIN_KIMASE_ST; 1.

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01-MAR-1989 (Rel.
15-JUL-1999 (Rel.
Protein kinase C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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[2]
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00130; DAG_PE-bind; 2. Pfam; PF00168; C2; 1. Pfam; PF00433; pkinase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR0002719; Euk_pkinase.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00130; DAG_PE-bind; 2.
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Ono Y., Fujii T., Ogita K., Kikkawa U.,
"The structure, expression, and propert
the protein kinase C family.";
J. Biol. Chem. 263:6927-6932(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M18331;
PIR; B28163; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P28867;
                                                                                                                                                                                                                                                                                                                                     PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.
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PHORBOL-ESTER
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RA George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA George R.A., Lewis S.E., Rahdrarg Q., Chen L.X.,
RA George R.A., Lewis S.E., Rahdrarg Q., Chen L.X.,
RA George R.A., Bayendale J., Bayenktaroglu L., Beiffer B.D.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson R.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dorbin K.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., McDerson D.,
McDarley G. McCharley G. McCharley G. McCharley J.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Nucleolar protein AT band 60B (Minifly protein).
NOP60B OR WFL OR CG3333.
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Drosophila melanogaster (Fruit fly):

Drosophila; Mettazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99189256; PubMed-10087258;
Giordano E., Peluso I., Senger S., Fu
"minifly, a Drosophila gene required
J. Cell Biol. 144:1123-1133(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99045289; PubMed-9829824; Phillips B., Billin A.N., Cadwell C Merriam J.R., Carbon J., Poole S.J.
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Baldwin D.,
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).
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P18714;
01-NOV-1990
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01-OCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Gastrula zinc finger protein XFG20-1 (XLCGF20.1).
                 MEDITINE-95094815; PubMed-8001572;
Schaefer U., Rausch O., Bouwmeester
"Sequence-specific recognition of a
zinc-finger protein in Xenopus.";
                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea.
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TIGRFAMS; TIGR00425; CBF5; 1.
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, Nelson K.A., Nixon
, Pittman G.S., Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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461
                                                                                                                                                                                             Xenopus.
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POLY-ALA.
POLY-LYS.
POLY-LYS.
POLY-LYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.5;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                               T., Pieler repetitive
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C outstation -
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Matches 12
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TRANSFAC; T02366;
Interpro; IPR000822; Znf_C2H2.

Pfam; PF00096; Zf-C2H2; 18.

PRINTS; PR00048; ZINCFINGER.

PRODOM; PD000003; Znf_C2H2; 18.

SMART; SM00355; ZnF_C2H2; 18.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 17.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 18.
                                                            UBPF_HUMAN STANDARW,

Q9Y4E8: Q9HCA6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
105quitin carboxyl-terminal hydrolase 15 (EC 3.1.
thiolesterase 15) (Ubiquitin-specific processing
                                                                                                                                                                   NAMUH_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Second-order repeats in Xenopus laevis finger proteins.";
J. Mol. Biol. 208:639-659(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 85-613 FROM N.A.
MEDLINE=90040698; PubMed=2509712;
N1etfeld W., El-Baradi T., Mentzel H.,
Poeting A., Knoechel W.;
                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                        ZN_FING
SEQUENCE FROM N.A.
                     NCBI_TaxID=9606
                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inc-finger;
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90 11
118 1,
146 1
174 1
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286
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675 AA;
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474
57
585
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642
77116 MW;
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112
140
168
                                Chordata;
Primates;
                                                                                                                                                                                                                                                                       28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inding; DNA-binding; B4 C2H2-TYPE.
                                                                                                                                                                                                                                                          Score 52; DB Pred. No. 28; 8; Mismatches
                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                        C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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C2H2-TYPE.
; 033094852C1FCF39 CRC64;
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                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.
18.
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                                                                                                                                                                                                                                                                      DB 1;
28;
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                                                                                     3.1.2.15) (Obiquitin sing protease 15)
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                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                 Length 675
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RESULT
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Best Local
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ACT_SITE
CONFLICT
CONFLICT
CONFLICT
                                                          KFMS_MOUSE STANDARD; PRT; 977 AA.

p09581; Q9DBH9;

10-mar-1989 (Rel. 10, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Macrophage colony stimulating factor I receptor precursor (CSF-1-R)

(EC 2.7.1.112) (Fms proto-oncogene) (c-fms).

CSF1R OR CSFMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kimura Y., Saya H., Nakao M.; "Cloning and identification of human Unph-2."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF013990; AAG28973.1;
EMBL; AB011101; BAA25455.1;
MEROPS; C19.022; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         code for large proteins in vitro."; DNA Res. 5:31-39(1998).
                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                  Mus musculus (Mouse)
                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00442; UCH-1; 1. Pfam; PF00443; UCH-2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences of The complete sequences of 100 new cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Ishikawa K.-I., Miyajima
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                   CT_SITE
                                                                                                                                                                                                                                                                                                                                                           l conjugation
T_SITE 219
T_SITE 804
T_SITE 812
NELICT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             placenta, liver, thymus, lung, and ovary, wi
expression in other tissues.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Ubiquitin ubiquitin + a thiol.
TISSUE SPECIFICITY: Expressed
                                                                                                                                                                                                                   576 EMETDEPDDESSQDQELPSENENSQSEDSVG
                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                           3 QSESSTPSTGGFSGKETPSEDDRSQSREHMG
                                                                                                                                                                                                                                                                                 Similarity
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PS00973; UCH_2_2; 1
PS50235; UCH_2_3; 1
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                                                                                                                                                                                                                                                                                                                                                                                                   pathway;
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H -> N (IN REF. 2
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                                                                                                                                                                                                                                                                     Pred. No. 39;
7; Mismatches
                                                                                                                                                                                                                                                                                             Score 52;
                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                               Thiol protease; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified human clones from brain v
                                                                                                                                                                                                                                                                                  DB 1;
39;
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                                                                                                                                                                                                                                                                                             Length 902
                                                                                                                                                                                                                                                                                                                        CRC64;
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brain which ca
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Frunon M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Frunon M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Barajuez I., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Washaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                             tyrosine phosphate.
-!- SUBCELUTAR LOCATION: Ty
-!- SIMILARITY: BELONGS TO T
PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 5 I
              wse by non-profit institutions as long as its content modified and this statement is not removed. Usage hor send an email to '' or send an email to ''
                                                                                                                                                                                                    This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van der Geer P., Hunter T.;

"Identification of tyrosine 706 in the kinase insert as the major colony-stimulating factor 1 (CSF-1)-stimulated autophosphorylation site in the CSF-1 receptor in a murine macrophage cell line.";

Mol. Cell. Biol. 10:2991-3002(1990)

-I- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN STIME RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue X., Favot P., Dunn T.L., Cassady A.I., Hume D.A.;
"Expression of mRNA encoding the macrophage colony-stimulating receptor (c-fms) is controlled by a constitutive promoter and t specific transcription elongation.";
specific transcription elongation.";
wol. Cell. Biol. 13:3191-3201(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wynshaw-Boris A., Yoshida K. Hayashizaki Y.; "Functional annotation of a Nature 409:685-690(2001).
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MEDLINE-88217329; PubMed-2966922;

Rothwell V.M., Rohrschneider L.R.;

"Murine c-fms cDNA: cloning, sequence analysis and retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTOPHOSPHORYLATION SITES.
MEDLINE 90258890; PubMed 2160591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93268269;
Yue X., Favot P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rothwell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP
                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.; PubMed=8497248; Dunn T.L., Cass
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CSF-1/PDGF
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MBL outstation -
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| tissue-
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Matches
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Pfam; PF00069; pkinase; 1
Pr00m; PF000001; Euk_pki
SMART; SM00410; IG_like;
SMART; SM00408; IGC2; 1.
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CARBOHYD
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CARBOHYD
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SMART; SM00410; IG_like; 3.

SMART; SM00408: IGC2; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00140; RECEPTOR_TYR_KIN_III; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X06368; CAA29666.1; ALT_SEQ
EMBL; AK004947; BAB23691.1; -
EMBL; S62219; -; NOT_ANNOTATED_CDS
PIR; S01880; TYMSMD.
HSSP; P11362; 1FGK.
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InterPro; IPR001824;
InterPro; IPR001245;
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                 QSESSTPSTGGFSGKE-----TPSEDDRSQSREHM
                                            imilarity
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                                                                                                                                                         302
335
389
410
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                                                                        AA;
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: Ig_like.
: RTKinaseIII.
: Tyr_pkinase.
                                          28.9%;
31.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat
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MISSING (IN REF. 1).
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PROTEIN
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                                   Pred. No. 43; '; Mismatches
                                           Score 52; DB
Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase;
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E C2-TYPE DOMAIN

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N KINASE.
                                                                                                                                                                                                                                                                                        SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                    11;
                                                    Length 977;
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Pfam; PF00047; ig; 4.

Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Euk_pkinase; 2.

SMART; SM00410; IG_like; 3.

SMART; SM00400; IGC2; 1.

SMART; SM00210; TYFKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00210; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00211; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _RAT
KFMS_RAT
                                                                                                                                                                                                                                                                                                                               InterPro; IPR003598; InterPro; IPR003600; InterPro; IPR001824; InterPro; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q00495;
Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-JUN-2002 (Rel. 41, Last annotation update)
Macrophage colony stimulating factor I receptor
(EC 2.7.1.112) (Fms proto-oncogene) (C-fms).
 DOMAIN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Wistar; TISSUE-Skeletal muscle; MEDLINE-93001225; PubMed-1389227; Borycki A.G., Guillier M., Leibovitch M.P., Le "Molecular cloning of CSF-1 receptor from rat analysis and regulation during myogenesis."; Growth Factors 6:209-218(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSF1R OR CSFMR OR FMS. Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X61479; CAA43706.1;
PIR; S16385; S16385.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                            Proto-oncogene; Tyrosine-protein kinase; Rev
Transferase; Glycoprotein; Phosphorylation;
                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719;
InterPro; IPR003006;
                                                                                                                                                                 [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS PROTEIN IS THE RECEPTOR TYROSINE-KINASE TRANSMEMBRANE RECEPTOR CATALYTIC ACTIVITY: ATP + a protein tyrtyposine phosphate.
SUBCELLULAR LOCATION: Type I membrane I SIMILARITY: BELONGS TO THE CSF-1/PDGF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE
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537
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204
299
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                                                                                                                                                                  domain;
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978
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503
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978
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; Ig_c2.
; Ig_like.
; RTKinaseIII.
; Tyr_pkinase.
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                                                                                                                                                                  Repeat
POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

IG-LIKE C2-TYPE DOMAIN 5.

IG-LIKE C2-TYPE DOMAIN 5.

IG-LIKE C3-TYPE DOMAIN 5.

PROTEIN KINASE.

ATP (BY SIMILARITY).
                                                                                                               RECEPTOR.
EXTRACELLULAR
                                                                                                                                        MACROPHAGE
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Sciurognathi; Muridae;
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                                                                                                                                                    SIMILARITY
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                                                                                                                (POTENTIAL).
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; Murinae; Rattus.
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Sequence
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Best Local S
Matches 12
PIR; JN0785; JARD.
PIR; JN0785; JARD.
HSSP; P07248; IARD.
InterPro; IPR000822; znf_C2H2.
Pfam; PF00096; zf-C2H2; 2.
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ACT_SITE
DISULFID
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DISULFID
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01-JUN-1994
16-OCT-2001
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SEQUENCE
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                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
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between
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                                     EMBL; L03811; AAA32690.1;
PIR; JN0785; JN0785.
HSSP; P07248; LARD.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=93366180; Pub Drysdale M.R., Kolze
                                                                                                                                                                                                                                                                                                                            CREA.
                                                                                                                                                                                                                                                                                                                                     DNA-binding
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                                                                                                                                                                                                                            creA.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
                                                                                                                                                                                                                                                                                                                  Aspergillus
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                                                                                                                                                                 FUNCTION: INVOLVED IN CARBON CATABOLITE
THE TRANSCRIPTION OF THE ALCR, ALCA AND
A GC-RICH REGION IN THEIR PROMOTER (BY SUBCELLULAR LOCATION: Nuclear:
SIMILARITY: BELONGS TO THE CREA/MIG GROUNDERS
                                                                                                                                                         FINGERS PROTEINS.
                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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olze S.E., Kelly J.M.;
niger carbon catabolite

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    Carbon catabolite r

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21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Short neurotoxin 1 precursor (Cobrotoxin).
Naja atra (Chinese cobra).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                    DISULFIDE BONDS.

DISULFIDE BONDS.

MEDLINE-71125117; PubMed-5533659;

Yang C.C., Yang H.J., Chiu R.H.C.;

Yang C.C., Yang disulfide bonds in cobro

Time position of disulfide bonds in cobro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chu R.C.,
Submitted
                                                                                                                                                                                                                         MEDLINE-93192268; PubMed-8448165; Chiou S.H., Raynor R.L., Zheng B., Chambers T.C., Kuo J.F.; Chiou S.H., Raynor R.L., Zheng B., Chambers and neurotoxin: "Cobra venom cardiotoxin (cytotoxin) isoforms and neurotoxin: comparative potency of protein kinase C inhibition and cancer cytotoxicity and modes of enzyme inhibition."; Biochemistry 32:2062-2067(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic structures of cardiotoxin 4 and cobrotoxin atra (Taiwan cobra).";
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DOMAIN
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Yang C.C., Yang H.J., Huang J.S.;
"The amino acid sequence of cobrotoxin.";
Biochim. Biophys. Acta 188:65-77(1969).
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Nuclear protein; Metal-binding.
Nuclear protein; Metal-
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PROSITE; PS50157; ZINC_FINGER_C2H2_2;
  MEDLINE=91065386;
Yu C., Lee C.-S.,
                                                 STRUCTURE BY NMR.
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Elapidae; Elapinae; Naja.
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, Yang C.C.;
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  PubMed=2249693;
Chuang L.-C., S
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Wang C.Y.;
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EMBL; U58520; AAB03223.1; --
EMBL; U58521; AAB03223.1; --
EMBL; U77490; AAB36930.1; --
EMBL; U77491; AAB36931.1; --
EMBL; U77492; AAB36931.1; --
EMBL; U74582; AAB01538.1; --
EMBL; U42582; AAB01538.1; --
EMBL; Y12492; CAA73097.2; --
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SEQUENCE
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Biochemistry 32:2131-2136(1993).
-i--FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC ACCEPTLICHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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Eur. J. Biochem.
[7]
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PROSITE; PS00272; SNAKE_TOXIN; 1.
Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene
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                                                                                                                                                                                         3D-structure.
                                                                                                                                                                                                                                                         InterPro
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TISSUE SPECIFICITY: Expressed by the venom gland.
MISCELLANEOUS: LD(50) IS 0.09 MG/KG BY SUBCUTANEOUS INJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SNAKE TOXIN FAMILY.
                                                                                                                                                                                                                                                     1COD; 20-JUL-95.
1COE; 20-JUL-95.
rPro; IPR003571; Snake_toxin.
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D40667; D40667.
 27
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                                                             Similarity
                        QSESSTPSTGGFSGKETPSEDDRSQSREHMG
 QQSSQTPTTTGCSGGETNCY - - KKRWRDHRG
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1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb
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## ALIGNMENTS

O9ULH6; Q96P46; 01-MAY-2000 (TERMBLrel. 13, Created) 01-MAY-2000 (TERMBLrel. 13, Last sequence update) 01-JUN-2002 (TERMBLrel. 21, Last annotation update) KINAL244 protein (BIG3) (Fragment).

Homo sapiens (Human).

KIAA1244

Q9ULH6

PRELIMINARY;

PRT;

1807 ⋛

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SOURCE TO BE RECTORDED TO SOURCE TO 
                                 Query Match
Best Local Similarity
    Matches
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                                                                                                                                                                                                                                                                                                              "KIĀA1244 as a novel distantly related member (BIG3) of the BIG1/Sec7p subfamily of ARF GEFs.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033070; BAA86558.1; -.
EMBL; AF413080; AAL04174.1; -.
                                                                                                                                                       SMART; SM00222; Sec7;
NON_TER 1
SEQUENCE 1807 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
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TISSUE=BRAIN;
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tive 0;
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Score 216; DB 4;
Pred. No. 6.8e-20;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl R., Catabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Humë D.A., Kamiya M., Lee N.H.,
A Gustluch M., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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01-DEC-2001
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Q9CR92;
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Mus musculus (Mouse).
**rrota; Metazoa; Chordata;
**rrota; Rodentia;
                                        Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilr
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
Nature
                                                                                                                                                                                                                                                                                                 MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J;
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"Functional annotation of a Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                               Hayashizaki Y.;
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(TrEMBLrel. 19, Last sequence update)
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Pred. No. 1.1e
0; Mismatches
             full-length mouse
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                                         .., Wilming
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Genomics 59:77-84(1999).
EMBL; AF117065; AAD38499 1.
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                                                                                                    STRAIN-FRIEDLIN;
Ivens A.C., Murphy L.,
Rajandream M.A., Barrel
Submitted (JUL-2001) to
                                                                                                                                                                                                                                                                      Hypothetical P1105.11.
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MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzad
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                         Q9NED2
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SMART; SM00298; CHROMO; 1.
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                                                    STRAIN-FRIEDLIN
                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                            5
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17; Conserv
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                                                                                                                                                                                                                                                                                   (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
L 119.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
(Created the control of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative'
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                                                                                                                          hy L., Quail
Barrell B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      den
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Primates;
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                Bagherzadeh
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7; Mismatches
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Pred. No. 1
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in Mismatches
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                                                                                                                                           Harris D., Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
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                Α.,
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                                                                                                                                             K., Lawson
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                  H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
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RESULT
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Best Local
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09V7N4;
01-MAY-2000
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01-JUN-2001
01-JUN-2001
01-JUN-2002
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EMBL; AL139794; CAB75569.1; -.
Hypothetical protein.
SEQUENCE 1114 AA; 119250 MW; I
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2001) to the
EMBL; BC005460; AAH05460.1;
HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99K50
                                                                                   SEQUENCE FROM N.A. STRAIN-BERKELEY:
                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                             CG4282 protein.
CG4282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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MGI:97286; NC1
                                                                                                                                                                                                                                                                                                                                                                                     193
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PS00030;
707 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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Last
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Last annotation update)
                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.5; D
Pred. No. 7.5;
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44B42C6E146E5D50 CRC64;
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annotation update)
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; Murinae; Mus
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Best Local
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01-JUN-2002
01-JUN-2002
01-JUN-2002
      Stapleton
                                                                                                                                                 CG4282
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                                   SEQUENCE FROM
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RA Beeson K.Y., Benos P.V., Berman B.P., Baylandari D., Bolshakov S., Ra Borkova D., Botchan M.R., Bouck J., Broktein P., Berottler P., Ra Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibaywam C., Matlai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., Lai Z., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Mullians G.S., Pan S., Pollard J., Purl V., Reese M.G., Ra Muthulov G., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Spier E., Siden K.A., Saunders R.D.C., Scheelar F., Shen H., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinserbach J., Walssenbach J., Purley K.C., Wu D., Yang S., Yao Q.A., Walssenbach J., Wang S., Yao Q.A., Ra Zheng X.H., Zhong F.N., Zhong W., Zhon W., Zhon S., Zhao Q., Zheng L., Ra Zheng X.H., Woyers E.W., Rubin G.M., Venter J.C., Shao Q., Zheng L., Ra J., Purley K.C., Wu D., Yang S., Yao Q.A., Walssenbach J., Walssenbach J., Walssenbach J., Wang S., Yao Q.A., Walssenbach J.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., M
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bes
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8
PROSITE; PS50157; ZINC_FINGER_C2H2_7;
DNA-binding; Metal-binding; Zinc-finger
SEQUENCE 642 AA; 74195 MW; F3B91AB91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00384; AT_hook; 1.
SMART; SM00355; ZnF_C2H2; 9
                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Eterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brandon R.C., Rogers Y.-H.C.,
                             STRAIN-BERKELEY;
                                                                                                                 NCBI_TaxID=7227;
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15; Conserv
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(TrEMBLrel.
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     Brokstein
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Last annotation update)
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Pred. No. 5.
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G., Helt G., Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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  Agbayani
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                                                                                                                                                                                                     Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                           Brachycera; Muscomorpha;
     Α.
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     Carlson
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asley E.M.,
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Benfey P.N. xoansion in

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Best Local :
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01-JUN-2002 (TrEMBLrel. 20, Last sequence update)
Hypothetical 49.1 kDa protein (Fragment).
Homo sapiens (Human).
Eukaryota; Metarora. "
                                                                                                                                                                                                                                                                             01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
MCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0048; ZINCFINGER.
Probom; PD000003; Znf_C2H2; 1.
SMART; SM00355; ZnF_C2H2; 8.
PROSITE; PS00011; GLU_CARBOXYLATION; U
PROSITE; PS00028; ZINC_FINGER_C2H2_1;
PROSITE; PS0157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019922; AAH19922.1; -
InterPro; IPR000294; VitK_dep_GLA.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 8.
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Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mung
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY069474; AAL39619.1; -
                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Hypothetical 153.9 kDa p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
   SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 AA;
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., Li P., Liao G., Miranda A., Mungall C.J.,
Paragas V., Park S., Phouanenavong S., Wan K.,
                                                                                                                                                                                                                                                   protein.
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01, Last sequence up
19, Last annotation
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7; Mi
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Pred. No.
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Pred. No. 5
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1; UNKNOWN_7.
2; 9.
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                                                                                          Arabidopsis
                                                                                                                                                     Embryophyta; Tracheophyta;
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                                                                                                                        core eudicots;
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                                                                                                                                                                                                         Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fung B., Fujii C.Y.,

RA Chung P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Chung P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Chung P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Huizar L.,

RA Gill J.E., Goldsmith A.D., Haas B., Hunser J.L., Shans N., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Alitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA G., Venter J.C., Davis R.W.;

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
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Best Local :
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O9C6Q6; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 210.0 kDa protein (Fragment).
T18124.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                     Utterback T., Van Aken S., Wu D., Yu G., Fraser C.M., "Sequence and analysis of c thaliana.";
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                                                                                          EMBL; AC079131;
                                                                                          Nature 408:816-820(2000).
EMBL; AC079131; AAG50770.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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   SEQUENCE
                                                             Hypothetical protein
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U191221; AAC49734.1;

U191222; AAC49734.1;

U19123; AAC49734.1;

U19124; AAC49734.1;

U19126; AAC49734.1;

U19127; AAC49734.1;

U19128; AAC49734.1;

U19129;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716
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12; Conserv
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   1854 AA;
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Hauser M.T., Feldmann K.A.,
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Pred. No.
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B. B., Hansen N.F., Hughes B., Huizar L.,
RA Gill J.E., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Miltscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,
RA Miltscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Willey D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Scoulence and Analysis of Chomocome 1 of the Clark Arabidocis
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Best Local S
Matches 12
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                                                                                                                                                                                                                   Q9QZX1
Q9QZX1;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9C727
Q9C727;
                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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MEDLINE-21016719; Pubmed-11130712;
Theologis A., Ecker J.R., Palm C.J.,
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnollophyta; eudicotytedons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                       Nucleolin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408:816-820(2000).
EMBL; AC073943; AAG50951.1;
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2599 AA;
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                            Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 40;
3; Mismatches
                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                        PRT;
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shbata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Query Match
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Matches 12
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SEQUENCE
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J. Biol. Chem. 274:27491-27496(1999).
EMBL; AF151373; AAD56625.1; -.
HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000504; RNA_rec_mot.
pfam; pF00076; rrm; 4.
SMART; SM00360; RRM; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYO;
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PROSITE: PS00030; RRM_RNP_1; UNKNOWN_3
SEQUENCE 715 AA; 77439 MW; 54A20FAI
                                                                                                                         "Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AK014457; BAB29364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai J., Shinagawa A., Shibata K.,
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SEQUENCE FROM N.A.
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Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and preliminary characterization of a calcium-binding protein closely related to nucleolin on the apical surface of inner medullary
                                                                                                       MGI:1921269; 3930402D05Rik.
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 l Similarity
12; Conser
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(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 17, Last annotation
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                                                                      ΑΑ,
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37.8%;
                  27.8%;
29.3%;
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                  Score 60;
Pred. No.
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RESULT 15
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Search completed: June 17, 2003, 11:59:44
Job time: 11.205 secs
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L MOI. Cell 5:181-187(2000).

R EMBL; AF143207; AAF36532.1; -.

R FlyBase; FBgn0026259; CIF2.

R InterPro; IPR0004161; EFTU_D2.

R InterPro; IPR000795; EF_GTPbind.

R InterPro; IPR0005225; Small_GTP.

R Pfam; PF00009; GTP_EFTU; 1.

R Pfam; PF00314; GTP_EFTU_D2; 2.

R PFINTS; PR00315; ELONGATNFCT.

R TIGRRAMS; TIGR00231; Small_GTP; 1.

R GTP-binding; Protein biosynthesis.

Q SEQUENCE 1144 AA; 127203 MW; A035415A3762CF0C CRC64;
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Best Local Similarity
Matches 14; Conserv
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O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 21, Last annotation update)
If2 protein.
If2 protein.
CIF2 OR CG10840.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20142670; PubMed=10678180;
Carrera P., Johnstone O., Nakamura A., Casanova J., Jackle H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9NJH7
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"VASA mediates translation through interaction with a Drosophila yIF2
                                                                          99 DDDEQDEPAAQESQSEE----EEKVVVSKPQKNEKKGKKAK 135
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                                                                                               1 EDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRAR 41 :||: :||: || || || ||: ||: ||:
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                                                                                                                                                        27.8%; Score 60; DB 5; Length 1144; 34.1%; Pred. No. 22; tive 10; Mismatches 13; Indels
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Q8XBF3
O64951
O64950
Q9SIS6
Q8S341
Q9L8P3
Q8TV49
                                                                                                                         Q96CH9
Q9ULH6
Q9BJE8
Q59301
                                                                                                                074491
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                                                                      Q9FT44
Q8U805
Q94IM7
Q929Z6
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        074491 schizosacch
Q9ft44 arabidopsis
Q80805 agrobacteri
Q941m7 hordeum vul
Q92926 listeria in
Q84bf3 escherichia
Q64951 tagetes ere
Q64950 tagetes ere
Q951s6 arabidopsis
Q86331 arabidopsis
Q86341 arabidopsis
                                                                                                                         Q96ch9 homo sapien
Q9ulh6 homo sapien
Q9bje8 plasmodium
Q59301 cellvibrio
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44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
52.5 52	52.5	۲	52.5	53	53	53	53	53	53	53	53	53	53	53	53	53.5	53.5	54	54			55	55	55	55	55	55.5
24.4	24.4	24.4	24.4	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.9	24.9	25.1	25.1	25.3	25.3	25.6	25.6	25.6	25.6	25.6	25.8
1289 196	895	769	234	900	729	528	488	462	462	423	410	373	259	186	176	1055	331	1048	732	673	555	654	351	.351	351	177	676
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Q9wz87 thermotoga Q9d068 mus musculu	~	Q8x1e4 neurospora	Q9s7c4 hevea brasi	Q9fk71 arabidopsis		Q9nuq3 homo sapien	Q9vff6 drosophila		007732 mycobacteri	Q9fk39 arabidopsis		Q8rue5 oryza sativ		Q9p0x1 homo sapien	Q9bjf0 plasmodium	Q9liv9 oryza sativ	Q93ex6 rhodococcus	œ	Q8vp74 pseudomonas			Q9fli2 arabidopsis	Q9mb29 nicotiana t	Q9smb7 nicotiana t	Q9smcl nicotiana r	O24127 nicotiana t	Q9n4t5 caenorhabdi

## ALIGNMENTS

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RESULT 2
Q9ULH6
ID Q9UL
AC Q9UL
DT 01-M
DT 01-M
DT 01-J
DE KIAA
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Q96CH9
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Best Local S
Matches 40
O9ULH6; Q96P46;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
KIAA1244 protein (BIG3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            д96Сн9;
                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (SEP-2001) to the
EMBL; BC014227; AAH14227.1;
                                                                                                                                                                                                                                                                                                                                                                     Hypothetical 66.4 kDa protein (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                              1 SPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYK 40
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40; Conserv
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ilarity 100.0%;
Conservative C
                                                                  PRELIMINARY;
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                                                                                                                                                                                    Score 215; DB 4
Pred. No. 6e-20;
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RESULT 4
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01-JUN-2001
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MEDLINE-21136462; PubMed-11237850;
Whattab A., Kun J., Deloron P., Kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2001)
EMBL; AB033070; BAA8
EMBL; AF413080; AAL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "KIAA1244 as a novel d
subfamily of ARF GEFs.
                                                                                                                                                                "Variants of Plasmodium falciparum Erythrocyte Expressed by Different Placental Parasites are Adhere to Chondroltin Sulfate A.";
J. Infect. Dis. 183:1165-1169(2001).
EMBL; AF334805; AAK28128.1; -.
                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata;
MCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N.,
"Prediction of the coding sequences of unidentified human of the complete sequences of 100 new cDNA clones from brain where the proteins in vitro.";
DNA Res. 6:337-345(1999).
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Mammalia; Eutheria;
                                                                                                                                    SEQUENCE
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Metazoa; Chordata; C
Metazoa; Primates; (
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ilarity 100.0%;
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AAL04174.1;
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Last annotation update)
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                                                                                            Score 65; DB 5
Pred. No. 0.89;
Mismatches
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Pred. No. 2.1e-19;
Mismatches 0;
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 PRT;
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Membrane Protein
Closely Related a
                                                                                                               Length 177;
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O74491; P78908;
O1-NOV-1998 (Tr)
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Pfam; PF00331; Glyco_hydro_10;
PRINTS; PR00134; GLHYDRLASE10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative ATP-dependent SPCC285.03.
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01-NOV-1998 (TrEMBLrel 08, Last sequence up
01-NAR-2002 (TrEMBLrel 20, Last annotation
Putative ATP-dependent RNA helicase C285.03)
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01-NOV-1996
                                                    Glycosidase; Hydrolase; Signal; Xylan
SIGNAL 1 19 POTENTIAL
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01-JUN-2002
                                                                                                                                                                                                                cdnas
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Yoshioka S., Kato
                                                                                                                                                                                                                                                                                                                                   STRAIN-PR745
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NCBI_TaxID=4896;
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InterPro; IPR001000; Glyco_h
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                            InterPro;
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   IPR001650;
                                  IPR000629;
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K., Nakai K., Okayama
f open reading frames
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Submitted (SEP-2000) to the
EMBL; AL392145; CAC08248.1;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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PS01090; TATD_2; UNKNOWN_1.
3306 AA; 368483 MW; 122B0D048E6C1E99
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ein; ATP-binding; Helicase;
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V -> Y (IN REF. 2).

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C (IN REF. 2).
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Garciadeblas B.;

"Plant cells express several stress calc sodium ArPase.";

Submitted (MAR-2001) to the EMBL/GenBank EMBL; AJ310845; CAC40033.1;

InterPro; IPR000661; H.K.Na/K.APAse. InterPro; IPR001454; Hlgnase/hydrlase. Pfam; PF00689; Cation_ATPase_C; 1.
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Q94 IM7;
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MEDLINE-21608550; PubMed=11743193;
Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Mood G.E., Almeida N.F., Jr., Woo L.
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmleri A.,
Rutyavin T., Levy R., Li M.-J., McClelland E., Romero P., Gordo
Raymond C., Rouse G., Saenphimmchok C., Wu Z., Romero P., Gordo
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan
Chumler F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., M. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mar Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub Cielo C., Slater S.; Company G., Com
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                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Str
Spermatophyta; Magnoliophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2323-2328(2001).
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InterPro: IPR002301; tRNA-synt_ile.
Pfam; PP00133; tRNA-synt_i; 1.
TIGRFAMs; TIGR00392; iles; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UPROSITE; PS00178; AA_TRNA_LIGASE_I; UPROSITE; PS00178; AA; 103781 MW; 5C6B8;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vascuroz-Baland T. A., Voca G. Vocales T., Constant D.,
Vascuroz-Baland T. A., Voca G.
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                                                          Q8XBF3;
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SEQUENCE FROM 11262 / SEROVAR 6A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative genomics of Listeria
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AL596171; CAC97357.1; -.
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                               (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73770 MW;
ii.
                                                                                                                                                                                                                                                  26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.0%;
29.0%;
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20,
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19,
21,
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                                                                                                                                                                                                                                     Score 57.5; D
Pred. No. 55;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence up
                               Created)
Last sequence update)
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wehland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25271A96C8558DBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                             -NAGNKIYTM-------AADKTISKLMTEY
                                                                                                                                                                                                                                                                                       lete proteome.
5C6B8BC1F21EDFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                 species.";
                                                                                                                                                                                                                                                                                                                UNKNOWN_1.
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                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cossart P.;
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                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                              Length 921;
                                                                                                                                                                                                                                      Indels
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RESULT
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Best Local :
                                                                                                                                                                                                                                                     064951;
01-AUG-1998
01-AUG-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE005413; AAG56916.1; --
EMBL; AE002559; BAB36061.1; ALT_INIT.
InterPro; IPR001451; Hexapep_transf.
Pfam; PF00132; hexapep; 3.
Transferase; Complete proteome.
SEQUENCE 201 AA; 22838 MW; 06E1F5
               PROSITE;
                                                                           del Villar Martinez A.A., Ma.R., Paredes-Lopez O.;
"Molecular Characterization of cDNAs Encoding 3-Hydroxy-3-
methylglutaryl Coenzyme A Reductase in Marigold (Tagetes erecta).";
J. Plant Physiol 155:205-211(1999).
                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicoty16 Asteridae; euasterids II; Asterales; Ast
                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3-hydroxy-3-methylglutaryl coenzyme A reductase.
                                                                                                                                                                                                                                                                                                           064951
                                                                                                                                                        Asteridae; euasterids
Helenieae; Tagetes.
NCBI_TaxID=13708;
                                                                                                                                                                                                                             Tagetes erecta (African marigold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perna N.T., Plunkett G. III, Burland V., Mau B., Glas
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpa
Posfai G., Hackett J., Klink S., Boutin A., Shao Y.,
Posfack E.J., Davis N.W., Lim A., Dimalanta E.T., Po
  SEQUENCE
                                          Pfam; PF00368;
                                                             J. Plant Physiol. 155:205-21
                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21074935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative serine acetlyltransferase of prophage CP-933T.
Z2984 OR ECS2638.
                                                     InterPro; IPR002202; HMG-CoA_red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
15; Conser
00368; HMG-COA_red; 1.
PS00066; HMG_COA_REDUCTASE_1; 1.
PS50065; HMG_COA_REDUCTASE_4; 1.
483 AA; 52816 MW; 850D4EA30A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           EKKQRNRNFLFWWRLANEMYINGNKLHKKAAKKLNSKIINKF 93
                                                                                                                                                                                                                                                                                                                                                                                                    EKKDPSRK-KEWWENA-----
                                                                                                                                                                                                                                                                             (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDL933 / ATCC 700927;
; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Enterobacteriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56.5;
Pred. No. 1
                                                                                                                                                                                   eptophyta; Embryophyta; Tracheop
  eudicotyledons; core eudicots;
erales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                           PRT;
 850D4EA30AD9AE70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   -GNKIYTMAADKTISKLMTEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06E1F5A1972A6CE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                           483
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                                                                                                                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kirkpatrick H.A.,
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                                                                                                                                                                                                               Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yokoyama K.,
Tobe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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Mismatches

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Indels Length

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26.3%; 33.3%;

Score Pred.

56.5; No. 3

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RESULT
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Best Loc
Matches
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Q9SIS6;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-MAY-2000 (TrEMBLrel. 13, Creat Ol-MAY-2000 (TrEMBLrel. 13, Last Ol-JUN-2002 (TrEMBLrel. 21, Last Putative purple acid phosphatase. AT2G01880.
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O64950;
O1-AUG-1998 (TrembLrel. O7, Created)
O1-AUG-1998 (TrembLrel. O7, Last sequence update)
O1-AUG-1998 (TrembLrel. O7, Last sequence update)
O1-JUN-3002 (TrembLrel. O7, Last annotation update)
O1-JUN-3002 (TrembLrel. 21, Last annotation update)
O1-JUN-3002 (TrembLrel. 21, Last annotation update)
O1-JUN-3002 (African marigold).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae; Helenieae; Tagotes.
NCBI_TaxID-13708;
        STRAIN-CV. COLUMBIA;

MEDLINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.;

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.;

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.

Cronin L.A., Shen M., VanAken S.E., Umayam L., Town C.R.
                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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PROSITE; F
PROSITE; F
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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del Villa
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"Molecular Characterization of cDNAs Encoding 3-Hydroxy-3-
methylglutaryl Coenzyme A Reductase in Marigold (Tagetes e)
J. Plant Physiol. 155:205-211(1999).
EMBL; AF034760; AAC15475.1; -.
InterPro; IPR002202; HMG-COA_red.
InterPro; IPR002302; HMG-COA_R_NADP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR00333; HMG_COA_R_NAD; 1.

PS00066; HMG_COA_REDUCTASE_1; 1.

PS00318; HMG_COA_REDUCTASE_2; ...

PS01192; HMG_COA_REDUCTASE_3; 1.

PS50065; HMG_COA_REDUCTASE_4; 1.

PS574 AA; 61862 MW; 435AA08R7308ALAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPKITTTTTTDQKKDPSQKKMKTSSKWWVEG3" OF TAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.3%;
33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No. 44;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence undate) annotation update
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RESULT 15
Q91L8p
ID Q91L8p
AC Q91L8p
DT 01-QC
DT 01-JU
DE CP4-5
OS Haemo
OC Bacte
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-: CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTI
ALCOHOL + PHOSPHATE.
EMBL; AC007069; AA021780.1; -
InterPro: IPR004843; M-ppestrase.
InterPro: IPR004844; S/T_phosphtse
InterPro: IPR000169; SHprot_acsite
InterPro: IPR000169; SHprot_acsite
InterPro: IPR0039; THIOL_PROTEASE_HIS; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                 Q9L8P3 PRELIMINARY; PR
Q9L8P3; O1-OCT-2000 (TrEMBLrel. 15, Crea
01-OCT-2000 (TrEMBLrel. 15, Last
01-JUN-2001 (TrEMBLrel. 17, Last
CP4-57 Integrase-like protein.
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01-JUN-2002
Purple acid |
PAP7.
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EMBL: AF492559; AAM15905.1; -
SEQUENCE 328 AA; 37549 MW; F897E0A8D39CA052 CRC64:
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Li D., Zhu H., Liu
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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ia; Proteobacteria;

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Haemophilus Bacter.

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OX NCBI_TaxID=727;
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RP SCOURNCE FROM N.A.
RC STRAIN=EAGAN;
RC STRAIN=EAGAN;
RX MEDLINE=20231799; pubMed=10768954;
RA Chang C.-C., Gilsdorf J.R., DiRita V.J., Marrs C.F.;
RA Chang C.-C., Gilsdorf J.R., DiRita V.J., Marrs C.F.;
RA Chang C.-C., Gilsdorf J.R., DiRita V.J., Marrs C.F.;
RA MEDLINE=20231799; pubMed=10768954;
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RA MEDLINE=20231799; pubMed=10768954;
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RA MEDLINE=20231799; pubMed=10768954;
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RA MEDLINE=20231799; pubMed=10768954;
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RA Chang C.-C., Gilsdorf J.R., DiRita V.J., Marrs C.F.;
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Listing first 45 summaries
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sp_vertebrate:*
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Ogwr66 caenorhabdi
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Ogwr76 drosophila
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## ALIGNMENTS

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Query Match 100.0%; Score 2698; DB 4; Length 1807; Best Local Similarity 100.0%; Pred. No. 3.4e-218; Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps	NON_TER 1 1 SEQUENCE 1807 AA; 199921 MW; B762C29916F72CB1 CRC64;	INCEPTO: 1PROU094; Sec/. SMART; SM00222; Sec7; 1.	EMBL; A1403000 AAL04174.1;	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.	SIGNAL 244 dS d HOVEL DISCHILLY TELECTED HEHIDEL (BIGS) OF THE BIG1/SECTED SUBSamily of ARE GEES.";	Hong W.;	SEQUENCE OF 38-1807 FROM N.A.	DNA Res. 6:33/-345(1999).	for large proteins in vitro.";	The complete sequences of 100 new cDNA clones from brain which code	"Prediction of the coding sequences of unidentified human genes. XV.	Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.,	MEDLINE=20039619: PubMed=10574462;	TISSUE-BRAIN	CHOITENCE EROM N A	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	KIAA1244	protein (BIG3)	(TrEMBLrel. 21,	01-MAY-2000 (TrembLiel. 13, Last sequence update)	3	Q9ULH6 PRELIMINARY; PRT; 1807 AA.	46	CT 1

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Matches 516
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 66.4 kDa protein (Fragment).
Homo sapiens (Human).
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0; Mismatches
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Catarrhini; Hominidae
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                                                                                                                                             RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Burnon G.G., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Berson D., Botchan M.R., Bouck J., Brokstein P., Bashkov S., Chandra I., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Center A., Chandra I., RA Gersty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., RA Gersty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dunn P., Bartis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., RA Glodek A., Gong F., Gorrell J.H., Gluz., Glabart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gluz., Gubart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Laukh G., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W444 PRELIMINARY;
Q9W444;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
CG5937 protein.
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
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Metazoa; Arthropoda; Tracheata;
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Ketchum K.A.,

Reese M.G.,

KTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHS PAVÉPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV PAVFPCISQLTCHVTDIRVRQAVREWLGRVGRVYDIIV ESAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ FSAGPELLRQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQ TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSGKE TPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAAD TAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKK 592 554 480 494 420 434 360 314 240 374

on update) Hexapoda; Insecta; Brachycera; Muscomorpha;

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RX MEDLINE=2019006; PubMed=10731132;
RX Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards G., Champe M., Henderson S.N.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Horil J.F., Royale R. J., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA George R.A., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
ENBL; AE003436; AAP46115.1;
-Fryenses Freenon2014. G5837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce
Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2000 (TrEMBLrel.
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CG9213.
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Interpro; IPR000904; Sec7.
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PROSITE; PS00583; PFKB_KIN
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RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA McIson D.R., Nelson K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Ponlard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Klamos I., Simpson M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
REMBL, AE003499; AAF48473.1; -.
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SEQUENCE
                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlsoń J., Chavez C., Dorsett V., Farfan D., Frise E., George R., Ghampe M., Chavez C., Dorsett V., Farfan D.A., Frise E., George R., Gonzalez M., Guarin H., Li P., Llao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K
                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                             Brachycera; Muscomorpha;
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Best Local S
Matches 66
                                                                                                                                                                       Matches
                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Charleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wallow, J., Paragas V., Park S., Phouanenavong S., Wallow, C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AV061596; AAL29144 1; -.
                                                                                                                                                                                                                                                    FlyBase; FBgn0032678; CG12750.
InterPro; IPR003891; IF_eIF4G_MA3.
InterPro; IPR003580; Protachykinin.
Pfam; PF02847; MA3; 1.
SMART; SM00203; TK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY061353; AAL28901.1; -. FlyBase; FeBpn0030655; CG9213. SEQUENCE 687 AA; 78148 MW; 7376BABC9E18EE76 CRC64;
                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
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        199
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                                                        141 IGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQV-KKVLFED-DERSTDSSQQCSS
                                                                                                      164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 QKPQDDDERQAKPHSSSSAQGSSRGWRKPGAKAPSPPRRSRSRSKSATSSDEEEEEAVQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 -- LVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFSG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVW 240
                                                                                                                                       85
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                                                                                                                                                                       , 68
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                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRPQHLMDQGQMRHSFSAGPELLRQDKRP-----RSGSTGSSLSVSVRDAEAQIQ 455
     EDEDIFEETAQVSP---PRGKEKRQWRARMPLLSVQPVSNADWVWLVKRLHKLCMELCNN 255
                                                                                                      EQRTYE----KFYGLLAQRFCNINKIYIPPFEEIFKDTYQTTHRLDTN-----RLRNVSK
                                                                                                                                     EEKTIQVPEAKLAGFL--RYISMQNLAV--IFDLLLDSYRTAREFDTSPGLKCLLKKVSG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----MTSESLLLKTFSRERKEPAKPNEKA--QQIDAYDPAKSGRELNPYWKSNGTGLPGF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKV---EKKGEPLGP----RGQDSPLL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SEDEKERKRRKKKSKRSRKESASEDEWVEAPPPLAADNVTKKEPPQRDDW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALAKKLEKPAKKSKKN-VSKHKSRSKSKSSKKSRKHRN----SSSSSESSTSSSSSF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQFESGREKDKARQELREAREAMLQQAKERAELRGQRERQKELR------GEADWML
                                   F--FAHLLFTDAISWDV----LECIQLNEDDTTSSSRIFIKILFQELAEYMGLGKLNAKL
                                                                                                                                                                                                                                        751 AA;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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22.1%;
                                                                                                                                                                                   4.8%;
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                                                                                                                                                                    57;
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Last sequence update)
Last annotation update)
                                                                                                                                                                    Score 130.5; DB 
Pred. No. 0.03; 
57; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133; DB Pred. No. 0.016
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L C.J.,
Wan K.,
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QΥ
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:   : :    STGQLHSKYSAHPLSSHQSQPVPESTSAEGEELLPSQPSVTPKFQPLMTQG 640	SETVAAKMISTGQLHSKYSAHPLSSHQ	581	Вb
DQGQMRH	DQGQMRHSFSA	, 411	Qy
RMKPQGKQSFSSTPESTAFEGSTSVDHMTLTLSQPMLQPYQEVPLE 580	LPTQFQPRMKPQGKQSFSSTPESTAF	527	Db
QHNLSAFPKEVKVEKKGEPLGPRGQDSPL	MTEYKKRKQ QHNLSAFP	365	Qy
	QPSGYPPQPSVKPSIKKEISLGAESAP	467	탕
SR	DPSRKKEWWENAGN	, 339	Qγ
LRSQSECQVLAEPEGVVAADWDILMQPPPRPRLEQEVSAGPELTVFEKSIAV 466	PTQTVKSRLRSQSECQVLAEPEGVVAADWDILMQP	407	Дb
DRSQSR-EHMGESLSLKAGGGDLLLPPSPKVEKK 338	GKETPSEDDRSQSR-EHMGESLSLKAGG	, 298	Qγ
PAMVNISGGPKKSGEPLS 406	1	385	Вþ
WLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGFS 297	WLVKRLHKLCMELCNNYIQMHLDLENCH	240	Qy
EKYES	EEKEVSTESSSYIEKYESSEDLSSSEQE	.330	멍
SSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWV 239	EDDERSTDSSQQCSSEDEDIFEET	184	γO
4.8%; Score 128.5; DB 11; Length 1306; y 19.3%; Pred. No. 0.098; rvative 51; Mismatches 123; Indels 203; Gaps 20;	4.8%; Sco 19.3%; Pro ive 51;	Query Match Best Local 9 Matches 9	
1306 a; 144102 MW; 6255CFD233456C19 CRC64;	1306 1306 1306 AA; 144102 MW; 625	NON_TER SEQUENCE	SOS
D6; AATRNA_ligaseII. AA_TRNA_LIGASE_II_2; UNKNOWN_1.	PS00339; AA_TRNA_LIGASE_II_	Inter PROSI	7 D D
01) to the EMBL/GenBank/DDBJ databases. NC42194.1; -	; 1 (APR-2001) to the 150395; CAC42194.1;		DR P. P.
		SEQUENCE	RR
se). 9; Chordata; Craniata; Vertebrata; Euteleostomi; 9; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	<pre>is (Mouse). Metazoa; Chordata; ( Sutheria; Rodentia; ( =10090;</pre>	Mus. musc Eukaryot Mammalia NCBI_Tax	8888
tein similar to human KIAA1210	ovel protein similar to		GN DE
urel. 19, Created) 3Lrel. 19, Last sequence update) 3Lrel. 20, Last annotation update)	(TremBLrel. 19, Creat (TremBLrel. 19, Last (TremBLrel. 20, Last	01-DEC-2001 01-DEC-2001 01-MAR-2002	222
MINARY; PRT; 1306 AA.	PRELIMINARY; PRT;		A I
		ω□	Q9 RE
SSGSEDSDKSTSESSDSSNSSSDESDAEPQ 499	SGSEDSDKSTSESS	468	Дb
77	MDQGQMRHSFSAGPELLRQDKRPRSGS	. 412	Qy
EKEQEKEKEKQRKSKKEKEKDKKRKKEEKKAAKKKSKRRKSQES 467		415	Дb
KTISKLMTEYKKRKQQHNLSAFPKEVKVE		352	γQ
SSEEDSSSDSSSESSSSSSSSSSSSSSSSSSSSSSS	SSEEDSSSDSSSESSS	358	Дb
ESLSLKAGGGDLL	GKETPSEDDRSQSREHMGESLSLKAGGG	298	γQ
:     ILANAGGNPFRDGSAPAGNT	:  :	312	Дb
GDPF		256	γQ
	: : :    :      KDDVLVESIAGLFPKDNPRNTR	269	DЬ

- RQDKRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPD

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017596;
01-JAN-1998 (TrEMBLrel. 0:
01-JAN-1998 (TrEMBLrel. 0:
01-MAR-2002 (TrEMBLrel. 2:
C25D7.3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C25D/.3.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000822; Znf_C2H2.

PROSTTE; PS00028; ZINC_FINCET_C2H2_1; 1.

DNA-binding; Metal-binding; Zinc-finger
SEQUENCE 2150 AA; 249768 MW; E6A29F205124B589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81039; CAB02774.1; -.
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                           TRGRPKKVKENLKKRIOPRRGQKEEAAHEPE-VVEEQEQVEPEVGPEVVHEPVPAPAAQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IERLSEDQLLGDQGSEDISFEEIQVDLLLESGVEVQVNQSVTISRSSTSFESLLVEDPEE
                                                  DKTISKLMTE-----YKKRKQQHNLSA-----FPKEVKVEKKGEP-----LGPR
                                                                                                        EYGELDEAGAPSPSEIVVHDEVLQDEVLQPNPKSSKKRGRRRKKTPPHIAKARKVFT---
                                                                                                                                                                                                                                                                                                                                                                                 SVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEP-----PIFKGDPFFILPS
--SISK--TEEIELAPTPTQQSRKRMANVSSEEATATRRQKRAKVEEPNDSDVSRVLTPE 1583
                                                                                                                                                                                                                   FETSPVPAPEGNIPSRAHSSDDDVQVISSETDPNGPINLVEQVQNDKLTAYQYSTEELLG
                                                                                                                                                                                                                                                                         FQSESSTPSTGGFSGKETPSEDD-----
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Pred. No. 0.48
3; Mismatches
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                                                                                                                                                                      GGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFP
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                            GDDALKRSSLTPTP---
                                                                            KEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGP--ELLRQDKRPRSGSTGS
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-TPMRQRMTEEEDPSEVDNSLQATPTKEQLRDELRSQCERLRT

RDRILA-LKAEIERRKQQAAAAVQM

383

441 357 ----RVIKEKEETPTPPPKP-----

203

211

189 143

260

263

323

----SFDELQQRLEASNRNMQHLHD

74

GPSPGEEKTIQVPE--AKLAGFLR-

101

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01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY047499; AAK77231.; FlyBase; FBgn0036365; CG10732.

SEQUENCE 809 AA; 89641 MW; 9B62B41AAF15FA81 CRC64;
                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
                      Similarity
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21,
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2; Mismatches
                    Score 122; DB
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                                                                                                                                                                                                                                                                                                            RX MEDILINE—20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., Ra Adams M.D., Chang Q., Chen L.X., Salton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ra Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Pfelffer B.D., Bandari D., Bolshakov S., Becson K.Y., Benos P.V., Berman B.P., Bandari D., Botshakov S., Ra Beeson K.Y., Benos P.V., Berman B.P., Bandari D., Botshakov S., Ra Berson K.Y., Benos P.V., Berman B.P., Bandari D., Botshakov S., Ra Berson K.Y., Benos P.V., Berman B.P., Bandari D., Botshakov S., Calley S., Dahlke C., Gadieu E., Center A., Chandra I., Ra Galdeu E., Center A., Chandra I., Ra Ballew R.M., Bouck J., Brokstein P., Dew I., Dietz S.M., Dowles B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Calley S., Dahlke C., Davenport L.B., Devies P., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H.; Gu Z., Guan P., Harris M. Glasser K., Ra Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Houth R., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Yolthan G.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Li J., Liang Y., Lin X., Li J., Ling Y., Lin X., Li J., Ling Y., Lin X., Li J., Ling Y., Lin X., Nather B., McInders R., Deng T., Woshrefi A., Noshrefi A
                                                                                                                                                       Query Match
Best Local
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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01-MAR-2001 (TremBLrel.
01-MAR-2001 (TremBLrel.
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se; FBgn0036365; CG10732
NCE 1657 AA; 183992 M
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      DVALSEMSDNRAQSIQSLHSVLETPTPDTTP---
                                                            DTQCSPKTPNNFDHAQSCQLIIELP-PDEKPNGHTKKSVSFREIVVSLLSHQVLLQNLYD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYEQKQRELEQRYVASNN
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                                                                                                                                                 4.5%;
21.1%;
                                                                                                                                                                                                                                            183992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16,
16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                 Score 122; DB Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last
                                                                                                                      Mismatches
                                                                                                                                                                                                                                      FF55F036A233ECBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
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a; Brachycera; Musc
                                                                                                                      181;
                                                                                                                                                                             5
   ----SFDELQQRLEASNRNMQHLHD 352
                                                                                                                                                                          Length 1657
                                                                                                                   Indels
                                                                                                                   140;
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                                                                                                                Gaps
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QRTFIT ID QRTFIT
ID QRTFIT
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                          Matches
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CLIB533; TRANSPOSON-LTR-RETROTRANSPOSON Neuveglise C., Feldmann H., Bon E., Gaillardin "Genomic evolution of the LTR-retrotransposons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces bayanus (Yeast) (Saccharo
Eukaryota; Fungi; Ascomycota; Saccharon
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8TF17 PRELIMINARY;
Q8TF17;
Q1-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ439550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
   676
                                                                                                                                                                                                                                   584 VTNMDVDSELQSKENITTESE--TNEINKPSNTDEDVYEENVYRIPTAIQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                          LTNQETITAEQVKKVLFEDDERSTDSSQQCSSEDEDIFEETAQVSPPRGKEKRQWRARMP
-LHDSTNDSVTITSKKDNLTDDKDLQSQQELFEKVS--
                                                      FQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPPSPKVEKKDPSRK 343
                                                                                                                LVGSQKTININNEDNI - - ASRMQKNISGNEINYKELSDDDSDCS:
                                                                                                                                                                          LLSVQP----VSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYEQKQRELEQRYVASNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGQMRHSFSAGP--ELLRQDKRPRSGSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNDV - - - TSELRAEAASLQKE - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFEDDERSTDSSQQCSSEDEDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EALKAQMARLKG---MLYTVSQIEESTPSMG--STLERRSEERTSVERELPAEIAQRVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -EEAAPAAPKERVVPVEYQRNVPIIR-QEAANA----AQRALHAQAM----INQKTADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQAKLLQIQNLAKTHLNEMERLRQQADSLPHNVNGGEAPKYESVQQVQDDMASLVGRMKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAR-2002) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1433
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAD29535.1;
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21,
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                                                                                                                                                                                                                                                                                                                                                    Score 116.5; 1
Pred. No. 1.2;
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Saccharomyces uvarum)
Saccharomycotina; Sacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87C4075851F039BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --------GPSPGEEKTIQVPE--AKLAGFLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                       142;
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C., Casaregola S.;
in hemiascomycetous
   ---DPEVLPEHMKIEKDVESQN 729
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 1433;
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441

635

593 323 538 263 489 203

Gaps

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                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; Pr00560; LRR; 8.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 3.
SMART; SM00369; LRR_TYP; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O8WZV3
O8WZV3
OBWZV73
O1WZV73
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Conserved hypothetical protein.
B7N14.260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AL669986; CAD21060.1; -
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Schulte U., Aign V., Hoheisel J., Brandt P., E
Schulte G., Mewes H.W., Mannhaupt G.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
 684
                          266
                                                       645
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SQPEPRIPVFD----FSRPSSRSEADAGDDADASNSSVRRKRQKPADSASSKRHSRMGSS
                       CMEEP--PIFKGDPFFILPSFQSESSTPSTGGFSG-----KETPSEDDRSQSREHMGES
                                                                                                                                                                                                                          LNDISDLNPEESLQASTPK-----RFPSVKIENWDDYEHVPAQVSGHISDEI--SPRTRS
                                                                                                                                                                                                                                                     LONLYDILLEEFVKGPSPGEEKTIQVPEAKLAGF--LRYISMONLAVIFDLLLDSYRTAR
                                                      NQFGAGVLDGYEFQDDFSYQSVGASG-----
                                                                                                             RRLSQYHDDTPGEQASSGQQTGDESPVHVSYMDSGGYLSPPKTHTRRGQETGQRKASVAV
                                                                                                                                       KVL--FEDDE---RSTDSSQQCSSEDE----DIFEETAQVSPP-----RGKEKRQWRARMPL
                                                                                                                                                                    AVPRIPNLSVSTKRVASSQQGAGSPLKLFQP--
                                                                                                                                                                                               EFDTSPGLKCLLKKVS----GIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETSSAPRIKTIYYNEAISRNADLKEKHAYKE 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFTALQPAVEPC-ISQLTCHVTDIRVRQAVRE 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFLNKAFNS - - - LNKKRKRPIENKT - SFNDTAKRDNKRQRK - - - - - - - - NIIKLLPDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKSKNNSDISISPKGNNEELVQ----LVDSNKAEKQDATLESSAITDEPIEIENPAANKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEKKGE---PLGPRGQDSPLLQRPQHLMDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDNETSQGVQFQPESIVTSSSDNDTQN--DDYSTDKESHHLPLVVNVMDNTDQTYDKPNK
                                                                                                                                                                                                                                                                                                                                        11 protein.
2309 AA; 252994 MW;
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                               4.3%; Score 115; DB 3; I
18:8%; Pred. No. 3;
tive 71; Mismatches 174;
                                                                                 LSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLEN-----
                                                                                                                                                                                                                                                                                                                                         583ACF6D3A12B67C CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fartmann B.,
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                                                                                                                                                                                                                                                                                                            Length 2309;
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                                                                                                                                                                   ----YDTFTSEILQ
                                                      - IEGDKENQGPNDD
                                                                                                                                                                                                                                                                                 164;
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                                                                                                                                                                                                                                                                                 Gaps
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 739
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QRTET71
ID QRTET71
AC QRTET7
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT EEG11
GN EEG1
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GN EEG1
GN EUKar
OC Homo
OC EUKar
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OX NCBLI
RN [1]
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Best Local Sim
Matches 106;
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OSTE71;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Aerbajinai W., Miller J.L.;
Submitted (JAN-2002) to the EMBL,
EMBL; AY074490; AAL71549.1; -.
SEQUENCE 1077 AA; 120974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEG1.
550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                NNFDHAQSCQ-----LIIELPPDEKP---NGHTKKSVSFREIVVSLLSHQVLLQNLYDIL
                                                                                                                                                                                                                                                                                                                                                                                                HNLEFAKELQKTFSGLSLDLLKAQKKAQRREHMLKLEAEKKKLRTILQVQYVLQNLTQEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSLKAGGGDLLLP-----WWEN
NNVESQKHSLTSQSQISPKSWGVATASLIPNDQLLPRKLNTEPKDVPKPVHQPVGSSSTL
                                                     KQETPKLWPVQLQKEQDPKKQTPKSWTPSMQSEQNTTKSWTTPMCEEQDSKQPETPKSWE
                                                                                                                                      KRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPFFILPSFQSESSTPSTGGF-----S
                                                                                                                                                                                                                                                    KKVLFEDDERSTDSSQQCSSEDEDIFE-ETAQVSP------
                                                                                                                                                                                                                                                                                                            YRTAREFDTSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPTPLQRSSLQKDGKKGRPPLTELITKPSSRPTRPSSKASSKGRTPKEHGGPGSAMNTDR
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                          ENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPL---GPRGQDSPL
                                                                                                             -----QRKQDTSKLRSTLPEEQKKQEISKSKP---SPSQWKQDTPKSKAGYVQEEQK 489
                                                                                                                                                                                                                                                                                 VQKDFKG---GLNGAVYLPSKELDYLIKFSKLTCPERNESLSVEDQMEQSSLYFWDLLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISPSPETQSMKLSYQQIQAAIEKRR------KEVHAEKHREQVEPGTPSGKDVPRPR
                                                                                                                                                                    ADYARKPNLPKRWDMLTEPDGQEKKQESFKSWEASGKHQEVSKPAVSLE-
                                                                                                                                                                                            -------PRGKEKRQ-----WRA-----RMPLLSVQPVSNADWVWLV
                                                                                                                                                                                                                          -EMLIQSEKKTQLSKTESVKESESLMEFAQPEIQPQEFLNRRYMTEVDYSNKQGEEQPWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.2%;
18.0%;
                                                                      ---SEDDRSQSREHMGESL-SLKAGGGDLLLPPSPKVEKKDPSRKKEWW
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21,
21,
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Best Local S
Matches 90
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SEQUENCE
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ProDom; PD000093; SH2; 1.
SMART; SM00462; PTB; 1.
SMART; SM00252; SH2; 1.
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"N-Shc: a neural-specific adapter molecule that mediates signaling
from neurotrophin/Trk to Ras/MAPK pathway.";
Oncogene 13:1111-1121(1996).
EMBL; D84361; BAA12322.1; -.
EMBL; D84361; BAA12323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00640; PID; Pfam; PF00017; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FAR-2002 (TrEMBLrel. 20, Last annotation update)
P64 isoform of N-SHC (P52 isoform of N-SHC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96404502; PubMed=8808684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iomo sapiens (Human)
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 403
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                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                               PS01179; PID;
PS50001; SH2;
SDIYSTPEGKLHVA-PTGEAPTYVNT-QQIPPQAWPAAVSS--AESSPRKDLFDMKPFED
                                                KMPPPGGFLDTRLKPRPHAPDTAQFAGKEQTYYQGR----
                                                                                                  LQCPTKIPALH-DRMQSLDEPW-
                                                                                                                                                  HMRSISFASGGDPDTTDYVAYVAKDPVNRRACHILECCDGLAQDVIGSIGQAFELRFKQY
                                                                                                                                                                            QVKKVLFED---
                                                                                                                                                                                                    CEAVPGAKGAFKKRKPPSKMLSSILGKSNLQFAGMSISLTISTASLNLRTPDSKQIIANH
                                                                                                                                                                                                                          FDTSPGLKCLLKK------VSGIGGAANL-YRQSAMSFNIYFHALVCAVLTNQETITAE 176
                                                                                                                                                                                                                                                                            PGEEKTIQVPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEAQ------TQAWTNMVLTVLNQIQILPDQT-----FTALQPAVF 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKDPVLRKEKLQDLMTQIQGTCNFMQ-ESVLDFDKPSSAIPTSQPPSATPGSPVASKEQN
                      GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPK
                                                                   -----FILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLS------LKAGG
                                                                                                                        RQWRARMPLLSVQPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPF
                                                                                                                                                                                                                                                   PGDEPLPRPPRGAPHASDQVLGPGVTYVVKYLGCIEVLRSMRSLDFSTRTQITREAISRV
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                                                                                                                                                                                                                                                                                                                                                     594 AA;
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                                                                                                                                                                                                                                                                                                                                                      64056 MW;
                                                                                                                                                                                                                                                                                                                4.1%;
18.5%;
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                                                                                                                                                                                                                                                                                                  71;
                                                                                                                                                                                                                                                                                                   Score 111; DB 4;
Pred. No. 0.95;
l; Mismatches 20!
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                                                                                                                                                                           -----DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEK 218
                                                                                                                                                                                                                                                                                                                                                     047A9D08002E41BF CRC64;
                                                                                                                                                                                                                                                                            -- AKLAGFLRYI-SMQNLAVIFDLLLDSYRTARE 124
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                                                                                                                                                                                                                                                                                                    205;
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                                                -HLGDTFGEDWQQTPLRQGS
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                                                                                                  -TEEEGDGSDHPYYNSIPS
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TAP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
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564 SHLINH 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHLINH 569
                        SQLTCH 493
                                                GDFLVRKSTTNPGSFVLTGMHNGQAK---
                                                                                                  ALKNQPLGPVLSKAASVECISPVSPRAPDAKMLEELQAETWYQGEMSRKEAEG--LLEKD
                                                                                                                          EVKVEKKG---
                                                                                                                                                  SDIYSTPEGKLHVA-PTGEAPTYVNT-QQIPPQAWPAAVSS--AESSPRKDLFDMKPFED
                                                                                                                                                                         GDLLLPPSPKVEKKDPSRKKEWWENAGNKIYTMAADKTISKLMTEYKKRKQQHNLSAFPK
                                                                                                                                                                                                    KMPPPGGFLDTRLKPRPHAPDTAQFAGKEQTYYQGR-----HLGDTFGEDWQQTPLRQGS
                                                                                                                                                                                                                                                                            ROWRARMPLLSVOPVSNADWVWLVKRLHKLCMELCNNYIQMHLDLENCMEEPPIFKGDPF 278
                                                                                                                                                                                                                                                                                                   HMRSISFASGGDPDTTDYVAYVTKDPVNRRACHILECCDGLAQDVIGSIGQAFELRFKQY
                                                                                                                                                                                                                                                                                                                            QVKKVLFED----
                                                                                                                                                                                                                                                                                                                                                   CEAVPGAKGAFKKRKPPSKMLSSILGKSNLQFAGMSISLTISTASLNLRTPDSKQIIANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQLTCH
                                                                       ----KRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQILPDQTFTALQPAVFPCI
                                                                                                                                                                                                                                                   LQCPTKIPALH-DRMQSLDEPW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594 AA;
                                                                                                                                                                                                                          ----FILPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLS-----LKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493
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EPLGPRGQDSPLLQRPQ-HLMDQGQMRHSFSAGPELLRQD

516 431 458 384 402

-HLLLVDPEGTIQT-KDRVFDSI

-----DERSTDSSQQCSSEDEDIFEETAQVSPPRGKEK

308

218 248

-TEEEGDGSDHPYYNSIPS

347

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Neuronal Shc.
Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata;
Theria; Primates;
                                                                                                                                                                                                                  Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC026314; AAH26314.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KRPRSGSTGSSLSVSVRDAEAQIQAWTNMVLTVLNQIQIILPDQTFTALQPAVFPCI 487
FDTSPGLKCLLKK------VSGIGGAANL-YRQSAMSFNIYFHALVCAVLTNQETITAE
                                       PGDEPLPRPPRGAPHASDQVLGPGVTYVVKYLGCIEVLRSMRSLDFSTRTQITREAISRV
                                                                          PGEEKTIQVPE--------AKLAGFLRYI-SMQNLAVIFDLLLDSYRTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDFLVRKSTTNPGSFVLTGMHNGQAK-------HLLLVDPEGTIRT-KDRVFDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALKNQPLGPVLSKAASVECISPVSPRAPDAKMLEELQAETWYQGEMSRKEAEG--LLEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVKVEKKG---
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                 64042 MW;
                                                                                                                                     4.1%; Score 111; DB 4; Length 594; 18.5%; Pred. No. 0.95;
                                                                                                            71;
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EPLGPRGQDSPLLQRPQ-HLMDQGQMRHSFSAGPELLRQD
                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                 FE484556345FF6C5
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594
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                                                                                                                    205;
                                                                                                                                                                                                 CRC64;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                    120;
                                                                                                                    Gaps
                                       188
                                                                            124
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Search completed: June 17, 2003, 11:59:43 Job time : 132.931 secs

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